

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
558	AE000392	Escherichia coli K-12 MG1655 section 282 of 400 of the complete genome	0.19	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-matc...	4.0
559	L81774	Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence	0.19	4001725	(AB015981) MnhA [Staphylococcus aureus]	3.0
560	AL021108	Drosophila melanogaster cosmid clone 137E7	0.19	4001688	(AB015718) protein kinase [Homo sapiens]	3.0
561	AB001510	Carabus leptolesioides mitochondrial DNA for NADH dehydrogenase subunit 5, partial cds	0.19	3758855	(Z98551) M.AL3P6.11 [Plasmodium falciparum]	2.4
562	AF069696	Egernia stokesii clone EST1 microsatellite	0.19	3328994	(AE001326) Amino Acid (Branched) Transport [Chlamydia trachomatis]	2.4
563	X64144	F.pringlei ppcA1 gene for phosphoenolpyruvate carboxylase	0.19	3242974	(AF069555) G protein-coupled receptor p2y3 [Meleagris gallopavo]	2.3
564	U56897	Human immunodeficiency virus type 1 gag polyprotein (gag) gene, partial cds	0.19	2257710	(U73041) resolvase-like protein [Thiobacillus ferrooxidans]	2.3
565	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.19	3874971	(Z99709) similar to NAD dependant epimerase/dehydratase family; cDNA EST EMBL:C10103 comes from this gene; cDNA EST EMBL:D66400 comes from this gene; cDNA EST EMBL:D70143 comes from this gene; cDNA EST yk493h11.3 comes from ...	1.8

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
566	Y12502	R.norvegicus mRNA for factor XIIIa	0.19	2133693	masquerade precursor - fruit fly (Drosophila melanogaster) >gi 665545 (U18130) masquerade [Drosophila melanogaster] >gi 1095942 prt 2110286A masquerade gene	1.8
567	S82470	BB1=malignant cell expression-enhanced gene/tumor progression-enhanced gene [human, UM-UC-9 bladder carcinoma cell line, mRNA, 1897 nt]	0.19	2444026	(U77783) N-methyl-D-aspartate receptor 2D subunit precursor [Homo sapiens]	1.8
568	U97408	Caenorhabditis elegans cosmid F48A9	0.19	542433	225K protein - Babesia bovis (fragment)	1.8
569	U10470	Pseudomonas fluorescens PHA depolymerase (phaZ) gene, complete cds.	0.19	3721862	(AB016024) Pfj2 (Plasmodium falciparum)	1.7
570	M88160	Ovis aries MAF214 locus polymorphic dinucleotide repeat	0.19	1293816	(U56963) T13A10.5 gene product (Caenorhabditis elegans)	1.4
571	AJ131336	mRNA for pollen allergen (Hol i 2, group II) > :: emb AJ131339 LIT13 1339 Lolium italicum mRNA for pollen allergen (Lol i 2, group II) > allergen (Poa p 2, group II) > :: emb AJ131338 TAE1 31338 Triticum aestivum mRNA for pollen allergen (Tri a 2, group II)	0.19	3880447	(AL032675) predicted using Genefinder	0.82
572	X84036	S.cerevisiae ARG8 and CDC33 genes	0.19	3882041	(AJ010405) hypothetical protein	0.62

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		Human WD protein			mucin - human >gi 501033	
573	U57058	IR10 pre-mRNA, partial cds	0.19	631302	(U14383) mucin [Homo sapiens]	0.60
574	AF034460	Penicillium thomii internal transcribed spacer 1, 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence; and 28S ribosomal RNA gene, partial sequence	0.19	114136	AMINO-ACID ACETYLTRANSFERASE Pseudomonas aeruginosa >gi 151036 (M38358) N-acetylglutamate synthase [Pseudomonas aeruginosa]	0.35
575	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.19	105270	alpha-2-adrenergic receptor - human name 'ADRA2R' [Homo sapiens]	0.27
576	AG001475	Homo sapiens genomic DNA, 21q region, clone: 125H6N2	0.19	94977	hypothetical protein 3 - Pseudomonas sp. (DSM 6898) plasmid pKB740 >gi 45867 (X66604) ORF3	0.16
577	M63284	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 9 and 10, clones lambda-Fc(3.2.93).	0.19	3024681	TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) of RNA polymerase II transcription factor TFIID [Homo sapiens]	0.088
578	U38241	Pseudomonas aeruginosa orotate phosphoribosyl transferase (pyrE), catabolite repression control protein (cre) and RNasePH (rph) genes, complete cds	0.19	3044086	(AF055904) unknown [Myxococcus xanthus]	0.052
579	AF039734	Lontra longicaudis transthyretin intron 1, partial sequence	0.19	322759	pistil extensin-like protein (clone pMG14) - common tobacco (fragment) >gi 19927 (Z14015) pistil extensin like protein [Nicotiana tabacum]	0.030
580	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.19	2147194	collagen - Paralvinella grasslei	0.002

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
581	AB004232	Drosophila melanogaster mRNA for DAD polypeptide, complete cds	0.19	2498765	PEROXISOMAL MEMBRANE PROTEIN PEX16 lipolytica]	0.002
582	AF098919	Gallus gallus alpha-globin gene domain 5' region	0.19	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-05
583	AE001457	Helicobacter pylori, strain J99 section 18 of 132 of the complete genome	0.19	2924552	(AL022018) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA264666; 2-match_description=LD08351.5p rime LD Drosophila melanoga...	3e-05
584	L10329	Plasmid RP4 traE gene, 3' end; traD gene, complete cds; traF gene, 5' end.	0.19	3878117	(Z49068) mitochondrial carrier protein	8e-07
585	AE001155	Borrelia burgdorferi (section 41 of 70) of the complete genome	0.19	861276	(U28739) similar to TPR domains in e.g. yeast STT1 protein [Caenorhabditis elegans]	2e-12
586	U49979	Orf virus E10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.19	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	1e-15
587	U88155	Xenopus laevis RanGTPase activating protein	0.19	995714	(X91258) pid:e198503 [Saccharomyces cerevisiae]	4e-16
588	AF061854	Schizosaccharomyces pombe Ctr4p (ctr4) gene, complete cds	0.19	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-19
589	M23865	S.cerevisiae CHS2 gene encoding chitin synthase.	0.18	<NONE>	<NONE>	<NONE>

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		Xenopus laevis XL- INCENP (XL- INCENP) mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
590	U95094					
591	AF067610	Caenorhabditis elegans cosmid F41A4	0.18	<NONE>	<NONE>	<NONE>
592	AF036329	Homo sapiens gonadotropin- releasing hormone precursor, second form (GnRH-II) gene, complete cds	0.18	<NONE>	<NONE>	<NONE>
593	Z49216	H.sapiens mitoxantrone- resistance associated mRNA	0.18	<NONE>	<NONE>	<NONE>
594	X02167	Torulopsis glabrata mitochondrial DNA for tRNA-Thr.-His and -Glu upstream of cytochrome b gene	0.18	<NONE>	<NONE>	<NONE>
595	Z31561	R.communis (Carmencita) Scr1 mRNA for sucrose carrier	0.18	<NONE>	<NONE>	<NONE>
596	L81692	Homo sapiens (subclone 2_c9 from P1 H56) DNA sequence	0.18	1346575	55 KD ERYTHROCYTE MEMBRANE PROTEIN	8.4
597	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L- cysteinyl-D-valine synthetase and isopenicillin N synthase	0.18	126404	SEED LIPOXYGENASE-2 (L- 2) soybean >gi170014 (J03211) lipoxygenase (EC 1.13.11.12)	6.5
598	U18315	Sus scrofa parathyroid receptor (PTH) mRNA, complete cds	0.18	1022323	(X04647) collagen alpha-2(IV) chain [Mus musculus]	3.8

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599	AL010158	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-85, complete sequence	0.18	2506816	VERSICAN CORE PROTEIN PRECURSOR PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE-BINDING PROTEIN) (GHAP) >gi 608515 (U16306) chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide	3.7
600	AB005287	Bos taurus mRNA for thrombospondin 1, complete cds	0.18	2146000	u0002b protein - Mycobacterium tuberculosis tuberculosis] >gi 1694863 gnl PID e283373 (Z33018) hypothetical protein Rv2968c [Mycobacterium tuberculosis]	2.9
601	AL021108	Drosophila melanogaster cosmid clone 137E7	0.18	3483032	(AL031371) hypothetical protein SC4G2.06 [Streptomyces coelicolor]	2.9
602	U57975	Danio rerio Notch homologue 3 mRNA, complete cds	0.18	85719	collagen alpha 1'(II) chain precursor - African clawed frog (AL021387) similar to Zinc finger, C4 type (two domains); cDNA EST yk452f4.5 comes from this gene; cDNA EST EMBL:T00774 comes from this gene receptor NHR-3 [Caenorhabditis elegans]	1.7
603	M30124	P.aeruginosa autonomously replicating sequence.	0.18	3878017	STEM CELL PROTEIN chicken >gi 62845 (X63371) transforming capacity [Gallus gallus]	1.3
604	X54965	G.sp alpha 5HR DNA	0.18	134304	(X98893) hTAFII68 [Homo sapiens] splicing [Homo sapiens]	1.3
605	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.18	1628403	92 KD TYPE IV COLLAGENASE PRECURSOR IV, 92K, precursor - rat >gi 1022784 (U36476) 92-kDa type IV collagenase [Rattus norvegicus]	1.2
606	U20793	Oryctolagus cuniculus renal sodium-dependent phosphate transporter type II mRNA, complete cds.	0.18	1705984		

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607	U23427	Human cholecystokinin type A receptor (CCK-A) gene, exons 1 and 2.	0.18	3261734	(Z94752) hypothetical protein Rv1004c	0.97
608	U49953	Rattus norvegicus protein kinase MUK2 mRNA, complete cds	0.18	551238	(X81847) pectate lyase 1 [Erwinia carotovora]	0.43
609	J00182	Human alpha globin gene cluster on chromosome 16: zeta gene.	0.18	1585259	traI gene [Amycolatopsis methanolica]	0.41
610	X62513	M.gallopavo gene for metallothionein	0.18	2494740	HYPOTHETICAL 28.3 KD PROTEIN IN GBD 5' REGION (ORF4) >gi 2120954 pir I39562 ORF4 - Alcaligenes eutrophus >gi 695274 (L36817) ORF4	0.31
611	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.18	86837	androgen receptor B - human	0.082
612	M12450	Rat vitamin D binding protein (DBP) mRNA, complete cds.	0.18	4210432	(AJ130783) APC2 protein [Mus musculus]	0.038
613	AF038539	Mus musculus muscle NSP-like 1 (Nspl1) mRNA, complete cds	0.18	3297877	(AJ224868) GNAS1 [Homo sapiens]	0.029
614	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.18	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.009
615	D38754	Pig mRNA for inter-alpha-trypsin inhibitor heavy-chain H1, complete cds	0.18	1397275	(U61947) C06G3.8 gene product [Caenorhabditis elegans]	7e-06

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616	X51508	Rabbit mRNA for aminopeptidase N (partial)	0.18	630864	LRR47 protein - fruit fly (Drosophila melanogaster) >gi 415947 (X75760) LRR47 [Drosophila melanogaster]	6e-07
617	X54850	S.kluyveri linear plasmid pSKL DNA for open reading frames 1-10	0.18	3183405	HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME I >gi 2370504 gnl PID e339194 pombe] >gi 3451305 gnl PID e1316730 (AL031324) very hypothetical protein [Schizosaccharomyces pombe]	2e-08
618	L21954	Human peripheral benzodiazepine receptor gene, exon 4.	0.18	3925211	(AL032626) cDNA EST EMBL:D70654 comes from this gene; cDNA EST EMBL:Z14359 comes from this gene; cDNA EST EMBL:D33409 comes from this gene; cDNA EST EMBL:D36239 comes from this gene; cDNA EST EMBL:Z14766 comes from this gene...	4e-09
619	U09355	Oryctolagus cuniculus protein phosphatase 2A1 B gamma subunit (skeletal muscle isolate) mRNA, complete cds.	0.18	3947877	(AL034382) putative mitosis and maintenance of ploidy protein [Schizosaccharomyces pombe]	8e-11
620	X58715	T.cruzi hsp70 mRNA for 70 kDa heat shock protein, partial cds	0.18	3024081	MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (MLCK) (CONTAINS: TELOKIN)	9e-12
621	AF060195	Mus musculus proteasome regulator PA28 beta subunit gene, complete cds	0.18	861276	(U28739) similar to TPR domains in e.g. yeast STI1 protein [Caenorhabditis elegans]	1e-14
622	L27235	Methylobacterium extorquens serine cycle proteins	0.18	2688949	(AF027208) AC133 antigen [Homo sapiens]	1e-14

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623	AF006573	Drosophila virilis maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.18	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-23
624	AF001782	Staphylococcus aureus strain SA502A AgrB	0.17	<NONE>	<NONE>	<NONE>
625	AJ223364	Homo sapiens germ-line DNA upstream of Jkappa locus	0.17	<NONE>	<NONE>	<NONE>
626	J03059	Human glucocerebrosidase (GCB) gene, complete cds	0.17	<NONE>	<NONE>	<NONE>
627	AB008860	Fugu rubripes Ca12 gene for pheromone receptor, complete cds	0.17	2198849	(AF004900) E3KARP [Homo sapiens] >gi 2665826 (AF035771) Na+/H+ exchanger regulatory factor 2 [Homo sapiens] factor 2 [Homo sapiens] >gi 3618353 gnl PID d1034182 exchanger isoform A3 [Homo sapiens]	7.8
628	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.17	539355	SCD25 protein (version 1) - yeast	7.5
629	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	482118	hypothetical protein C15H7.1 - Caenorhabditis elegans	4.5

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630	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.17	465932	HYPOTHETICAL 85.2 KB PROTEIN F58A4.11 IN CHROMOSOME III >gi 3874287 gnl PID e1344088 EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ... EMBL:C11886 comes from this gene; cDNA EST EMBL:C12577 comes from this gene; cDNA EST yk227e7.5 comes from this gene; cDNA EST yk303d1.5 comes from this gene; cDNA EST yk314c12.5 comes from this gene; cDNA ...	4.4
631	X55065	Chinese hamster metallothionein II gene	0.17	3687237	(AC005169) putative Cys3His zinc-finger protein	1.5
632	U15280	Rattus norvegicus oxytocin receptor (OTR) gene, exon 3 and complete cds	0.17	542565	cyclin E type II - fruit fly (Drosophila melanogaster) >gi 429168 (X75027) Drosophila cyclin E type II [Drosophila melanogaster]	0.45
633	X04862	Goat embryonic alpha globin gene zeta exons 2-3	0.17	86837	androgen receptor B - human	0.080
634	AL010222	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence	0.17	1177322	(X95466) CPG2 protein [Rattus norvegicus] >gi 1588593 prf 2208498A plasticity-related gene [Rattus norvegicus]	7e-07
635	X60111	H.sapiens mRNA for MRP-1	0.17	3237306	(U92715) breast cancer antiestrogen resistance 3 protein	3e-09
636	U49979	Orf virus F10R homolog gene, partial cds, and DNA polymerase gene, complete cds	0.17	3850072	(AL033385) dna-directed ma polymerase iii subunit [Schizosaccharomyces pombe]	7e-15

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637	AF006573	<i>Drosophila virilis</i> maltase 1 (Mav1) and maltase 2 (Mav2) genes, complete cds	0.17	2500558	PUTATIVE RIBONUCLEASE III (RNASE III) >gi 3876420 gnl PID e1346063 (Z81070) similar to ribonuclease [Caenorhabditis elegans]	2e-29
638	AE001141	<i>Borrelia burgdorferi</i> (section 27 of 70) of the complete genome	0.16	1850327	(U52370) fertilin beta [Homo sapiens]	2.3
639	M72980	<i>Anthonomus grandis</i> vitellogenin gene (VTG), complete cds	0.12	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	2e-56
640	AF023532	<i>Simulium vittatum</i> ATPase 6 gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.11	<NONE>	<NONE>	<NONE>
641	U76523	<i>Sambucus nigra</i> lectin precursor mRNA, complete cds	0.10	3482965	(AL031369) putative protein	0.49
642	AJ001596	<i>Danio rerio</i> mRNA for opioid receptor homologue	0.099	1706694	LANOSTEROL SYNTHASE 5.4.99.7) - fission yeast (<i>Schizosaccharomyces pombe</i>)	2.3
643	U26341	<i>Oryctolagus cuniculus</i> Na and Cl dependent betaine transporter mRNA, complete cds	0.099	2645804	(AF033381) betaine homocysteine methyl transferase [<i>Mus musculus</i>]	0.59
644	M11633	Bacteriophage Cp-5 (<i>S.pneumoniae</i>) 3' inverted terminal repeat	0.082	2314695	(AE000649) type IIS restriction enzyme R and M protein	4.3
645	X74103	<i>Streptomyces</i> sp. gene for alkaline serine protease I	0.073	1314734	(U54641) 220 kDa silk protein [<i>Chironomus thummi</i>]	6.3

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		Caenorhabditis elegans cosmid F32G8, complete sequence [Caenorhabditis elegans]	0.072	<NONE>	<NONE>	<NONE>
646	Z72509					
647	X70282	X.laevis xanf-1 gene	0.070	3851202	(AC005954) ZO-3 [Homo sapiens] [Homo sapiens]	0.40
		Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.069	<NONE>	<NONE>	<NONE>
648	Z69906					
649	AF056940	Drosophila virilis retrotransposon Tv1, complete sequence	0.069	2246532	(U93872) ORF 73, contains large complex repeat CR 73	5e-12
650	AJ001151	Homo sapiens genomic sequence	0.068	<NONE>	<NONE>	<NONE>
651	X54453	Bacteriophage BF23 gene 17 and gene 18	0.067	<NONE>	<NONE>	<NONE>
		P.pinea internal transcribed spacers 1 & 2 of ribosomal DNA	0.067	2459733	(U95374) aldehyde dehydrogenase [Haloferax volcanii]	4.3
652	X87936					
653	AF019236	Dictyostelium discoideum TipD (tipD) gene, complete cds	0.067	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1
		O.cuniculus mRNA for p53 protein	0.067	1703275	METHIONINE AMINOPEPTIDASE 2 (METAP 2) GLYCOPROTEIN (P67)	0.29
654	X90592					
655	U41805	Mus musculus putative T1/ST2 receptor binding protein precursor mRNA, partial cds	0.067	642518	(U17326) neuronal nitric oxide synthase [Homo sapiens]	0.29
		Homo sapiens KIAA0421 mRNA, partial cds	0.066	<NONE>	<NONE>	<NONE>
656	AB007881					
		Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-109, complete sequence	0.066	<NONE>	<NONE>	<NONE>
657	AL010213					

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658	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.066	1082461	homeotic protein HB9 - human	0.38
659	AF104156	Rattus exulans isolate huahine30 mitochondrial D-loop, partial sequence	0.066	1002380	(U24189) RRM-type RNA binding protein [Caenorhabditis elegans]	0.29
660	X97581	M.musculus mRNA for spalt transcription factor	0.066	4107313	(AL035075) putative myosin heavy chain	0.28
661	D85378	Human clone H20 N-acetylglucosaminyltransferase III DNA, exon 2	0.066	2114473	(U96963) p140mDia [Mus musculus]	0.22
662	M97561	Human (clone LA179) chromosome 21 sequence.	0.065	<NONE>	<NONE>	<NONE>
663	AE001373	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence	0.065	<NONE>	<NONE>	<NONE>
664	S75479	growth hormone receptor, growth hormone binding protein (GHR/BP gene) [mice, C57 black/6, Genomic, 179 nt, segment 8 of 10]	0.065	<NONE>	<NONE>	<NONE>
665	AF032922	Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds	0.065	3061308	(AB006074) topoisomerase III [Mus musculus]	0.82
666	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.065	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.12

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	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
667	X59552	G.domesticus mRNA for ventricular myosin heavy chain	0.065	2497098	HYPOTHETICAL 74.2 KD PROTEIN IN AMD1-RAD52 INTERGENIC REGION >gi 1077180 pir S49745 probable membrane protein YML034w - yeast (Saccharomyces cerevisiae) >gi 575685 (Z46659) unknown orf, len: 656, CAI: 0.13 [Saccharomyces cerevisiae]	0.014
668	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.065	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	5e-33
669	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
670	M30039	Sheeppox virus strain KS-1 ORF HM1 gene, partial cds; ORF HM2 and ORF HM3 genes, complete cds; and ORF HM4 gene, partial cds	0.064	<NONE>	<NONE>	<NONE>
671	Z68013	Caenorhabditis elegans cosmid W02H3, complete sequence [Caenorhabditis elegans]	0.064	<NONE>	<NONE>	<NONE>
672	AF041332	Bodo saltans unknown mRNA, kinetoplast gene encoding kinetoplast protein, complete cds	0.064	<NONE>	<NONE>	<NONE>
673	J00451	Mouse germline IgG-3 chain gene, D-J-C region, and switch region.	0.064	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
674	U41289	Dictyostelium discoideum K7 kinesin-like protein mRNA, complete cds	0.064	3482972	(AL031369) putative protein	9.3
675	M37395	L.lactis (strain SK11) proteinase plasmid pSK111 DNA, complete cds.	0.064	993019	(X87246) alternative start codon [Pseudorabies virus]	9.2
676	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb L01652 HUMVM LC Human ventricular myosin light chain 2 gene, seven exons.	0.064	730343	PROLACTIN RECEPTOR PRECURSOR (PRL-R) mouse >gi 220576 gnl PID d1001535 (D10214) prolactin receptor precursor [Mus musculus] >gi 293770 (L14811) prolactin receptor [Mus musculus] >gi 347842 (L13593) prolactin receptor [Mus musculus] receptor:ISOTYPE=long form [Mus musculus]	9.1
677	Z12021	G.max gene for catalase	0.064	2498711	ORIGIN RECOGNITION COMPLEX PROTEIN, SUBUNIT 2 >gi 1185461 (U38472) essential ORC2-related fission replication factor Orp2 [Schizosaccharomyces pombe]	5.3
678	L05668	Entamoeba histolytica protein serine/threonine kinase (pstkl) gene, complete cds.	0.064	733140	(U22453) carboxypeptidase [Simulium vittatum]	5.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
679	U50715	Mus musculus alpha-galactosidase A gene, complete cds	0.064	125398	HYGROMYCIN-B KINASE (HYGROMYCIN B PHOSPHOTRANSFERASE) (APH(7")) >gi 66885 pir WGSMHH hygromycin B phosphotransferase (EC 2.7.1.-) Streptomyces hygroscopicus >gi 581682 (X03615) pot. hyg protein [Streptomyces hygroscopicus] phosphotransferase [synthetic construct] >gi 2739064 cloning vector] >gi 2739068 (AF025747) hygromycin B phosphotransferase [unidentified cloning vector]	2.3
680	Z28182	S.cerevisiae chromosome XI reading frame ORF YKL182w	0.064	1079035	Om(2D) protein - fruit fly (Drosophila ananassae) >gi 443770 gnl PID d1006095 (D26553) ORF	1.8
681	M29917	Human ornithine aminotransferase gene, exon 1.	0.064	2317934	(U97553) unknown [murine herpesvirus 68]	1.4
682	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.064	861404	(U29154) T07F12.3 gene product [Caenorhabditis elegans]	0.47
683	AB014546	Homo sapiens mRNA for KIAA0646 protein, complete cds	0.064	1708118	HOMEBOX PROTEIN HB9 >gi 507425	0.35
684	AB010427	Homo sapiens mRNA for NORI-1, complete cds	0.064	2388676	(AF015539) precollagen P [Mytilus edulis]	0.018
685	U34774	Orf virus ankyrin-like repeat protein, F11L homolog, and F12L homolog genes, complete cds.	0.064	731668	SSF1 PROTEIN >gi 626624 pir S46700 SSF1 protein - yeast (Saccharomyces cerevisiae)	1e-05
686	AF022861	Mus musculus neuropilin-2(a5) mRNA, alternatively spliced, complete cds	0.064	4091978	(AF073359) benzaldehyde dehydrogenase [Pseudomonas sp. DJ77]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
687	U14331	Sus scrofa myogenin gene, complete cds	0.064	2781386	(AC004010) similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	3e-33
688	AF074870	Chironomus pallidivittatus clone 1219 non-telomeric Ssp repeat sequence	0.063	<NONE>	<NONE>	<NONE>
689	Z25523	H.sapiens repeat region DNA.	0.063	<NONE>	<NONE>	<NONE>
690	AE001378	Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence	0.063	<NONE>	<NONE>	<NONE>
691	Z72947	S.cerevisiae chromosome VII reading frame ORF YGR162w	0.063	<NONE>	<NONE>	<NONE>
692	Y14723	Choanophthalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.063	<NONE>	<NONE>	<NONE>
693	X74103	Streptomyces sp. gene for alkaline serine protease I	0.063	1730713	HYPOTHETICAL 108.5 KD PROTEIN IN UME3-PUB1 INTERGENIC REGION >gi 2131866 pir S62935 hypothetical protein YNL023c - yeast (Saccharomyces cerevisiae) >gi 1301855 gnl PID e239870 (271299) ORF YNL023c [Saccharomyces cerevisiae]	6.7
694	AF039843	Homo sapiens Sprouty 2 (SPRY2) mRNA, complete cds	0.063	232217	GLUTATHIONE S-TRANSFERASE GST-6.0 (GST B1-1) >gi 421198 pir S29772 glutathione transferase (EC 2.5.1.18) - Proteus mirabilis >gi 2126142 pir S71882 glutathione transferase (EC 2.5.1.18) B - Proteus mirabilis >gi 1053076 (U38482)	5.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
695	M63650	Mouse M-twist gene mRNA, complete cds.	0.063	1730141	FRAGILE X MENTAL RETARDATION SYNDROME RELATED PROTEIN 2 >gi 2135129 pir S60173 fragile X mental retardation syndrome related protein - human >gi 1098637 (U31501) fragile X mental retardation syndrome related protein [Homo sapiens]	1.8
696	Y13298	Homo sapiens GDP dissociation inhibitor beta pseudogene	0.063	1085930	hypothetical protein 4 - fowl adenovirus 1	1.3
697	X56600	Rat SOD-2 gene for manganese-containing superoxide dismutase	0.063	3882143	(AB018254) KIAA0711 protein [Homo sapiens]	0.60
698	Z23107	M.musculus mRNA for 5HTx serotonin receptor	0.063	1708162	HUNTINGTIN (HUNTINGTON'S DISEASE PROTEIN HOMOLOG) (HD PROTEIN)	0.45
699	M20670	Plasmodium vivax circumsporozoite protein gene, 3' end.	0.063	4033395	DNA GYRASE SUBUNIT B subunit [Mycobacterium xanthus]	0.35
700	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.r1a.	0.063	1350911	RETINOIC ACID RECEPTOR RXR-BETA sapiens >gi 3172498 (AF065396) retinoic X receptor B dJ1033B10.11 (Retinoid X receptor beta (RXRB)) [Homo sapiens] >gi 4249766 (AF120161) retinoic X receptor beta	0.16
701	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	2981200	(AF048732) cyclin T2b [Homo sapiens]	0.090
702	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.063	3877951	(Z81555) predicted using Genefinder	6e-07
703	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.063	3393018	(AL031174) hypothetical protein	2e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		E.coli genomic DNA.				
704	D90872	Kohara clone #419(54.7-55.1 min.)	0.063	2498198	CYTOCHROME B561 (CYTOCHROME B-561)	3e-19
705	M25528	M.crystallinum ferredoxin-NADP+ reductase (fnrA) mRNA, complete cds.	0.062	<NONE>	<NONE>	<NONE>
706	U45256	Strongyloides ratti microsatellite B DNA	0.062	<NONE>	<NONE>	<NONE>
707	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.062	<NONE>	<NONE>	<NONE>
708	AF044317	Homo sapiens TEL/AML1 fusion gene, partial sequence	0.062	<NONE>	<NONE>	<NONE>
709	Z73975	Caenorhabditis elegans cosmid T06E8, complete sequence [Caenorhabditis elegans]	0.062	3108187	(AC004663) Notch 3 [Homo sapiens]	2.9
710	X54232	Human mRNA for heparan sulfate proteoglycan	0.062	1076741	chitinase (EC 3.2.1.14) precursor - rice precursor - rice >gi 807955 (X87109) chitinase [Oryza sativa]	0.59
711	X03073	Bovine retinal mRNA for transducin beta-subunit	0.062	477578	sialidase - Actinomyces viscosus >gi 141852	0.087
712	Y12573	D.melanogaster Jun and 14-3-3 zeta gene	0.062	3879551	(Z70756) similar to collagen	0.073
713	L26573	Bombus terrestris mitochondrial cytochrome oxidase I, partial cds.	0.062	1684959	(U20600) NADH dehydrogenase subunit [Vanda lamellata]	0.039

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
714	U58994	Human ladinin (LAD) gene, complete cds	0.062	2811078	AMINOPEPTIDASE B (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B) >gi 2039143 (U61696) aminopeptidase B [Rattus norvegicus]	9e-06
715	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.062	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206) HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID e243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	5e-10
716	L16898	Mus musculus collagen alpha 1 type XVIII mRNA, 5'end.	0.062	1723657	(Z49907) B0491.1 [Caenorhabditis elegans]	1e-14
717	X99343	M.tuberculosis guaA/B & choD genes	0.062	3873807	(Z49907) B0491.1 [Caenorhabditis elegans]	2e-19
718	AF010193	Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds	0.061	<NONE>	<NONE>	<NONE>
719	L10182	Myrmeleon sp. 18S ribosomal RNA.	0.061	<NONE>	<NONE>	<NONE>
720	Y14723	Choanomphalus incertus mitochondrial cytochrome c oxidase subunit I gene, partial	0.061	<NONE>	<NONE>	<NONE>
721	L27840	Bovine respiratory syncytial virus nucleoprotein mRNA, complete cds.	0.061	542955	nucleoporin p62 - human	8.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
722	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.061	494454	Sus scrofa >gi 494455 pdb IPOS B Sus scrofa Sus scrofa >gi 1421210 pdb 1PCP Porcine Spasmolytic Protein (Psp) (Nmr, 19 Structures) Spasmolytic Polypeptide >gi 1633061 pdb 2PSP B Chain B, Porcine Pancreatic Spasmolytic Polypeptide	2.9
723	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.061	3845272	(AE001417) hypothetical protein [Plasmodium falciparum]	1.3
724	U26463	Sporidiobolus salmonicolor NADPH-dependent aldehyde reductase gene, complete cds	0.061	1710288	(U79302) unknown [Homo sapiens]	0.44
725	AF035443	Xenopus laevis weel homolog mRNA, complete cds	0.061	3979720	EMBL:D33048 comes from this gene; cDNA EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E... >gi 3979816 gnl PID e1358315 EST EMBL:D35780 comes from this gene; cDNA EST yk442c6.3 comes from this gene; cDNA EST yk442c6.5 comes from this gene; cDNA EST yk398f6.3 comes from this gene; cDNA E...	2e-04
726	Z48584	Caenorhabditis elegans cosmid ZK1321, complete sequence [Caenorhabditis elegans]	0.061	3183491	HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME III >gi 1065510 (U40419) C27F2.7 gene product [Caenorhabditis elegans]	3e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 32.0 KD	
727	X61489	Zea mays pep gene for (C3 type) phosphoenolpyruvate carboxylase	0.061	2496887	PROTEIN C09F5.2 IN CHROMOSOME III >gi 732538 (U22832) C09F5.2 gene product [Caenorhabditis elegans]	1e-15
728	AF025408	Drosophila melanogaster Windbeutel (wind) gene, complete cds	0.061	3702295	(AC005783) R33083_1 [Homo sapiens]	2e-60
729	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.060	<NONE>	<NONE>	<NONE>
730	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
731	Y08682	H.sapiens mRNA for carnitine palmitoyltransferase I type I	0.060	3319446	(AF077541) contains similarity to class-I aminoacyl-tRNA synthetases [Caenorhabditis elegans]	8.1
732	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.060	1041119	(D78016) TRAE [Enterococcus faecalis]	8.1
733	AF064030	Helianthus tuberosus lectin 2 mRNA, complete cds	0.060	632209	regulatory protein Rex - primate T-lymphotropic virus PTLV-L (fragment)	3.7
734	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.060	3098348	(AF037401) neuropeptide Y/peptide YY receptor Yc [Danio rerio]	2.1
735	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.060	125978	LAR PROTEIN PRECURSOR (LEUKOCYTE ANTIGEN RELATED) >gi 70146 pir TDHULK leukocyte antigen-related protein precursor - human >gi 34267 sapiens]	1.2
736	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.060	2055394	(U87306) transmembrane receptor UNC5H2 [Rattus norvegicus]	0.32
737	U69668	Human nuclear pore complex-associated protein TPR	0.060	4127854	(Y14063) ChT1 thymocyte antigen [Gallus gallus]	9e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
738	AB014553	Homo sapiens mRNA for KIAA0653 protein, partial cds	0.060	1326350	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	1e-09
739	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.060	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	5e-10
740	Z96260	H.sapiens telomeric DNA sequence, clone 12QTEL101, read 12QTELOO101.seq	0.059	<NONE>	<NONE>	<NONE>
741	M93128	Mouse homeobox protein (EVX2) mRNA, complete cds.	0.059	<NONE>	<NONE>	<NONE>
742	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.059	1652318	(D90904) lysostaphin [Synechocystis sp.]	4.7
743	AB007920	Homo sapiens mRNA for KIAA0451 protein, complete cds	0.059	479491	transcription factor brn-3b - human	0.71
744	M60445	Human histidine decarboxylase (HDC) mRNA, complete cds	0.058	<NONE>	<NONE>	<NONE>
745	U01836	Ustilago maydis exodeoxyribonuclease (REC1) gene, complete cds.	0.058	1171908	OLIGOPEPTIDE TRANSPORT SYSTEM PERMEASE PROTEIN OPPC >gi 1075086 pir D64184 oligopeptide transport system permease protein (oppC)C homolog - Haemophilus influenzae (strain Rd KW20) permease protein (oppC) [Haemophilus influenzae Rd]	1.5
746	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	0.058	3193265	(AF069131) chitinase [Bacillus subtilis]	0.002
747	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.057	433385	(U03978) dynein heavy chain isotype 7A [Tripneustes gratilla]	3.4

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.056	<NONE>	<NONE>	<NONE>
748	AJ005813	Lagopus lagopus genomic microsatellite sequence. LLST-4	0.056	3328678	(AE001299) hypothetical protein [Chlamydia trachomatis]	4.3
749	Y16828	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.055	<NONE>	<NONE>	<NONE>
750	AF012899	Sambucus nigra hevein-like protein mRNA, complete cds	0.055	137339	69 KD PROTEIN >gi 94375 pir S19150 hypothetical protein, 69K - turnip yellow mosaic virus	0.69
751	AF074385	Sambucus nigra lectin precursor mRNA, complete cds	0.035	<NONE>	<NONE>	<NONE>
752	U76523	Human retrovirus-like sequence-isoleucine c	0.034	<NONE>	<NONE>	<NONE>
753	M92069	GIL=ankyrin-like repeat [orf virus OV, NZ2, Genomic, 1608 nt]	0.033	2804465	(AF043700) contains similarity to human RNA-binding protein FUS/TLS (SW:Q28009) [Caenorhabditis elegans]	0.15
754	S78516	Chicken myosin alkali light chain mRNA, complete cds, clone pF1.	0.027	3334221	4-HYDROXYPHENYLPYRUVA TE DIOXYGENASE 4-hydroxyphenylpyruvate dioxygenase [Mycosphaerella graminicola]	6e-17
755	M15646	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.025	3877815	(Z96048) predicted using Genefinder	5.0
756	AF027174					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
757	AJ002291	Streptococcus pneumoniae pbp1b gene, complete	0.025	3880487	(Z68014) similar to ribose-phosphate pyrophosphokinase; cDNA EST EMBL:D73173 comes from this gene; cDNA EST EMBL:D70909 comes from this gene; cDNA EST EMBL:D73449 comes from this gene; cDNA EST EMBL:D76167 comes from this ge...	1.7
758	X79104	C.borulinum (NCTC 7272 type A) HA-33 and P-21 genes.	0.024	2648615	(AE000970) tungsten formylmethanofuran dehydrogenase, subunit B (fwdB 2) [Archaeoglobus fulgidus]	6.1
759	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.024	1663698	(D83785) expressed ubiquitously; product similar to D.melanogaster mam protein. [Homo sapiens]	4.7
760	U36197	Chlamydomonas reinhardtii cobalamin-independent methionine synthase mRNA, complete cds	0.024	585723	PEROXISOME PROLIFERATOR ACTIVATED RECEPTOR GAMMA (PPAR-GAMMA) >gi 233818 pir C42214 peroxisome proliferator-activated receptor gamma chain - African clawed frog >gi 214668 (M84163) peroxisome proliferator activated receptor gamma [Xenopus laevis]	0.42
761	L38865	Macaca mulatta (clone MMVA63) T-cell receptor alpha (TCR A) mRNA, partial cds.	0.023	<NONE>	<NONE>	<NONE>
762	AF035948	Mus musculus insulin receptor substrate-3 S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	2500587	SPLICEOSOME ASSOCIATED PROTEIN 49 spliceosome-associated protein SAP-49 - human >gi 556217	0.40
763	X98890		0.023	110072	proline-rich protein MP4 - mouse >gi 53182	0.18

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
764	X91212	L.esculentum mRNA for HD-ZIP protein	0.022	<NONE>	<NONE>	<NONE>
765	AC004498	Homo sapiens chromosome 5, P1 clone 1209C1 (LBNL H104), complete sequence [Homo sapiens]	0.022	<NONE>	<NONE>	<NONE>
766	U07083	Human prostatic acid phosphatase (ACPP) gene, exon 1	0.022	<NONE>	<NONE>	<NONE>
767	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.022	<NONE>	<NONE>	<NONE>
768	X56488	L.esculentum LAT59 gene 5' flanking region, expressed during pollen maturation	0.022	<NONE>	<NONE>	<NONE>
769	M34651	Pseudorabies virus with upstream and downstream sequences.	0.022	<NONE>	<NONE>	<NONE>
770	X66727	P.taeda gene for protochlorophyllide reductase	0.022	3878517	(Z92806) K10G4.4 [Caenorhabditis elegans]	4.3
771	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.022	1854452	(D89501) similar to salivary proline-rich protein P-B [Homo sapiens]	4.3
772	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	0.022	3021699	(AB005298) BAI 2 [Homo sapiens]	0.64
773	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.022	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi 9916 (X56203) liver stage antigen	0.058
774	X87369	C.perfringens nanH gene & ORF1.2.3 & 4	0.022	2062407	(U78975) poly(ADP-ribose) glycohydrolase [Bos taurus]	0.056

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
775	Y14971	Gallus gallus mRNA for K60 protein	0.022	134091	UT SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP 70 KD) >gi 85864 pir S02016 U1 snRNP 70K protein - African clawed frog >gi 65179 (X12430) U1 70K [Xenopus laevis]	0.032
776	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
777	AF003133	Caenorhabditis elegans cosmid T21E3	0.022	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-08
778	U57645	Human helix-loop-helix proteins Id-1 (ID-1) and Id-1' (ID-1) genes, complete cds	0.021	<NONE>	<NONE>	<NONE>
779	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	<NONE>	<NONE>	<NONE>
780	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
781	L04787	Borrelia hermsii outer membrane lipoprotein	0.021	<NONE>	<NONE>	<NONE>
782	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
783	L36890	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr1 (tRNA-Thr) gene; transfer RNA-Val (tRNA-Val) gene; oxi2 gene, complete cds; ORF2 and origin of replication (ori5).	0.021	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
784	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.021	<NONE>	<NONE>	<NONE>
785	M87504	Tetrahymena thermophila histone H3 (HHT2) gene, complete cds	0.021	<NONE>	<NONE>	<NONE>
786	U94346	Human calpain-like protease (htra-3) mRNA, complete cds	0.021	<NONE>	<NONE>	<NONE>
787	L01584	Trypanosoma cruzi calcium-binding protein (CUB2.8) gene, complete cds.	0.021	<NONE>	<NONE>	<NONE>
788	U36530	Pongo pygmaeus C1 microsatellite, clone #1, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	0.021	<NONE>	<NONE>	<NONE>
789	X03833	Human gene for interleukin 1 alpha (IL-1 alpha)	0.021	416974	EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT	8.9
790	U20806	Dictyostelium discoideum guanine nucleotide-binding protein alpha subunit 5 (G alpha 5) gene, complete cds.	0.021	1401211	(U58510) RNA helicase homolog [Chlorarachnion CCMP621]	8.8
791	Z59258	H.sapiens CpG DNA, clone 13d2, reverse read cpg13d2.rtlc.	0.021	3121732	ACONITATE HYDRATASE (CITRATE HYDRO-LYASE) (ACONITASE) >gi 2183256 (AF002133) aconitase [Mycobacterium avium]	7.0
792	AF030692	Plasmodium falciparum strain 7G8 chloroquine resistance candidate protein (cg2) gene, complete cds	0.021	3024190	NINE PROTEIN >gi 2120251 pir S66581 hypothetical protein 56 - phage 82 >gi 1051114 (X92588) orf56; related to nin60 (ninE) of bacteriophage lambda	5.8
793	U67570	Methanococcus jannaschii section 112 of 150 of the complete genome	0.021	2341037	(AC000104) F19P19.17 [Arabidopsis thaliana]	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
794	D86566	Human DNA for NOTCH4, partial cds	0.021	1708619	NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT-10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT]	3.1
795	L11648	Streptomyces coelicolor sigma factor (rpoX) gene, complete cds.	0.021	79833	hypothetical 119.5K protein (uvrA region) - Micrococcus luteus	1.8
796	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.021	128000	NEUROENDOCRINE CONVERTASE 1 PRECURSOR (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) propeptide processing protease [Mus cookii]	1.0
797	U30938	Rattus norvegicus microtubule-associated protein 2	0.021	468600	(X74416) beta-3 integrin [Takifugu rubripes]	1.0
798	D82364	Chicken mRNA for TSC-22 variant, complete cds, clone SLFEST52	0.021	693723	27 kda amelogenin [alternatively spliced]	0.61
799	U40041	Gallus gallus eHAND mRNA, complete cds	0.021	3449308	(AB011541) MEGF8 [Homo sapiens]	0.21
800	X71932	H.sapiens XB gene for tenascin-X, intron 14	0.021	627059	liver stage antigen LSA-1 - Plasmodium falciparum >gi 9916 (X56203) liver stage antigen	0.054
801	AF042333	Oryza sativa 24-methylene lophenol C24(1)methyltransferase mRNA, complete cds	0.021	854065	(X83413) U88 [Human herpesvirus 6]	0.014
802	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	0.021	3334377	TRANSMEMBRANE PROTEASE, SERINE 2	1e-05
803	AF003133	Caenorhabditis elegans cosmid T21E3	0.021	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	3e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
804	X57689	Rabbit mRNA for calcium channel BI-2 (lambda CBP109 and CB101)	0.021	2959370	(AL022117) hypothetical protein	1e-10
805	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.021	1109830	(U41534) coded for by C. elegans cDNA CEESI42F; Similar to helicases of SNF2/RAD54 family. [Caenorhabditis elegans]	5e-11
806	X77753	H.sapiens TROP-2 gene	0.021	1723657	HYPOTHETICAL 38.5 KD PROTEIN IN ERV1-GLS2 INTERGENIC REGION >gi 2132587 pir S64322 probable membrane protein YGR031w - yeast (Saccharomyces cerevisiae) >gi 1323010 gnl PID c243277 (Z72816) ORF YGR031w [Saccharomyces cerevisiae]	5e-11
807	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.021	2137872	zinc finger protein PZF - mouse >gi 453376	2e-19
808	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
809	AJ224935	Homo sapiens Promotor Region and PCK2 gene	0.020	<NONE>	<NONE>	<NONE>
810	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
811	X99941	A.thaliana GBF1 gene	0.020	<NONE>	<NONE>	<NONE>
812	X65138	M.musculus mRNA for tyrosine kinase >:: gb S57168 S57168 Sek=Eph-related receptor protein tyrosine kinase [mice, mRNA, 4242 nt]	0.020	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
813	L04787	<i>Borrelia hermsii</i> outer membrane lipoprotein	0.020	<NONE>	<NONE>	<NONE>
814	AJ223633	<i>Enterococcus faecium</i> genes encoding enterocin L50A and enterocin L50B plus 5' and 3' flanking regions	0.020	<NONE>	<NONE>	<NONE>
815	AB012106	<i>Brassica rapa</i> mRNA for SRK45, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AE001539	<i>Helicobacter pylori</i> , strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [<i>Saccharomyces cerevisiae</i>]	8.4
817	AF074386	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.020	94173	pol polyprotein - Chinese hamster intracisternal A-particle CHIAP34	8.0
818	M55264	Herpesvirus saimiri dihydrofolate reductase (DHFR) and snRNA (HSUR) genes, complete cds.	0.020	2924250	(Z98745) dJ29K1.2 [<i>Homo sapiens</i>]	6.5
819	AF052163	<i>Homo sapiens</i> clone 24456 mRNA sequence	0.020	1706288	D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR) >gi 2119482 pir I49246 D4 dopamine receptor - mouse >gi 758427 (U19880) D4 dopamine receptor [<i>Mus musculus</i>] >gi 1095539 prf 2109259A dopamine D4 receptor [<i>Mus musculus</i>]	4.9
820	AF074387	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.020	2113798	(Z83259) <i>AmphiBrf38</i> [<i>Branchiostoma floridae</i>]	4.7
821	AF052163	<i>Homo sapiens</i> clone 24456 mRNA sequence	0.020	3874733	(Z67754) cDNA EST EMBL:T02354 comes from this gene; cDNA EST EMBL:D32698 comes from this gene; cDNA EST EMBL:D35411 comes from this gene	4.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
822	L11002	Rat ankyrin binding glycoprotein-1 related mRNA sequence.	0.020	552132	(K01664) Bkm-like protein [Drosophila melanogaster]	3.8
823	AE001539	Helicobacter pylori, strain J99 section 100 of 132 of the complete genome	0.020	172292	(L11895) transmembrane protein [Saccharomyces cerevisiae]	3.8
824	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.020	3879798	(Z01120) similar to ttrK Domain (2 domains); cDNA EST yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37... >gi 3880220 gnl PID e1349842 yk390b10.3 comes from this gene; cDNA EST EMBL:D71652 comes from this gene; cDNA EST yk275f8.3 comes from this gene; cDNA EST yk393b9.3 comes from this gene; cDNA EST yk37...	1.3
825	U97519	Homo sapiens podocalyxin-like protein mRNA, complete cds	0.020	1345633	C1-TETRAHYDROFOLATE SYNTHASE, CYTOPLASMIC (C1-THF SYNTHASE) (METHYLENETETRAHYDROFOLATE DEHYDROGENASE / METHENYL TETRAHYDROFOLATE CYCLOHYDROLASE C1-tetrahydrofolate synthase [Rattus norvegicus]	0.066
826	AF003133	Caenorhabditis elegans cosmid T21E3	0.020	1709997	DNA REPAIR PROTEIN RAD18 >gi 1150622 protein rad18 [Schizosaccharomyces pombe]	2e-07
827	U32857	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence	0.019	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					NEUROGENIC LOCUS	
828	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.019	2506381	NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) mammary gene mRNA, complete cds.], gene product [Mus musculus]	3.3
829	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	0.019	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T008...	6e-15
830	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.018	<NONE>	<NONE>	<NONE>
831	U24578	Human RPI and complement C4B precursor (C4B) genes, partial cds.	0.013	478673	proline-rich protein precursor - kidney bean vulgaris]	3.1
832	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.011	<NONE>	<NONE>	<NONE>
833	U57649	Dibenzofuran-degrading bacterium DPO360 2,3-dihydroxybiphenyl 1,2-dioxygenase (bphC) gene, complete cds and 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoic acid hydrolase	0.011	<NONE>	<NONE>	<NONE>
834	X15642	Z.mays gene for phosphoenolpyruvate carboxylase	0.011	<NONE>	<NONE>	<NONE>
835	X51623	C.elegans collagen gene col-13	0.010	1695686	(D83706) pyruvate carboxylase [Bacillus stearothermophilus]	3.1
836	U83656	Rattus norvegicus NF-KB gene, promotor region	0.008	4240195	(AB020660) KIAA0853 protein [Homo sapiens]	10.0

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
837	AJ222657	Homo sapiens gene encoding retina-specific guanylyl cyclase	0.008	417704	POL POLYPROTEIN (ORF1A/1B) [CONTAINS: RNA-DIRECTED RNA POLYMERASE; HELICASE; PROTEASE]	7.4
838	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.008	544024	CHLORIDE CHANNEL PROTEIN, SKELETAL MUSCLE (CHLORIDE CHANNEL PROTEIN 1) (CLC-1) human >gi 397143 (Z25587) human CLC-1 muscle chloride channel [Homo sapiens] >gi 398161 (Z25884) human CLC-1 muscle chloride channel [Homo sapiens]	4.6
839	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	532468	(U13643) similar to reverse transcriptase; possible pseudogene [Caenorhabditis elegans]	3.8
840	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.008	4101160	(AF002589) cytochrome oxidase I [Austrofundulus limnaeus]	2.7
841	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	0.008	1711520	SRB-8/9 PROTEIN >gi 1334996	1.6
842	U48734	Human non-muscle alpha-actinin mRNA, complete cds	0.008	2829922	(AC002291) extensin [Arabidopsis thaliana]	0.11
843	U66669	Homo sapiens 3-hydroxyisobutyryl-coenzyme A hydrolase mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
844	D16492	Mouse mRNA for P100 serine protease of Ra-reactive factor (RaRF), complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human				
845	D90923	immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds, isolate 03S	0.007	<NONE>	<NONE>	<NONE>
846	AB011087	Homo sapiens mRNA for KIAA0515 protein, partial cds	0.007	<NONE>	<NONE>	<NONE>
847	AE000688	Aquifex acolicus section 20 of 109 of the complete genome	0.007	<NONE>	<NONE>	<NONE>
848	X63723	B.bovis WC1.1 mRNA	0.007	<NONE>	<NONE>	<NONE>
849	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
850	J00097	Human beta globin region Alu repetitive sequence type T.	0.007	<NONE>	<NONE>	<NONE>
851	D90923	Human immunodeficiency virus type 1 proviral DNA for envelope glycoprotein, partial cds, isolate 03S	0.007	<NONE>	<NONE>	<NONE>
852	U95094	Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
853	X91618	T.castaneum hunchback gene	0.007	<NONE>	<NONE>	<NONE>
854	X03838	Rat nontranscribed spacer (NTS) downstream of 28S rRNA gene	0.007	<NONE>	<NONE>	<NONE>
855	M55049	Rattus norvegicus interleukin-2 receptor alpha chain (CD25) mRNA, complete cds.	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
856	Z64318	H.sapiens CpG DNA, clone 9e2, reverse read cpg9e2.r1a.	0.007	<NONE>	<NONE>	<NONE>
857	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
858	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
859	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
860	X95276	P.falciparum complete gene map of plastid-like DNA	0.007	<NONE>	<NONE>	<NONE>
861	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
862	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>
863	AB000383	Leucania seperata nuclear polyhedrosis virus DNA for p13, ie, envelope protein, complete cds	0.007	<NONE>	<NONE>	<NONE>
864	D86566	Human DNA for NOTCH4, partial cds	0.007	<NONE>	<NONE>	<NONE>
865	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
866	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	3047072	(AF058825) No definition line found [Arabidopsis thaliana]	8.9
867	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.007	975754	(U29359) SpaO [Salmonella enterica]	8.6
868	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4
869	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	2499568	PROTEIN-L-ISOASPARTATE(D-ASPARTATE) O-METHYLTRANSFERASE (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL/D-ASPARTYL METHYLTRANSFERASE) methyltransferase [Drosophila melanogaster] >gi 1171337 melanogaster]	8.3
870	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	4092077	(AF095353) toll-like receptor 4 mutant [Mus musculus]	6.2
871	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	151377	(M80653) tetraheme [Pseudomonas stutzeri]	6.2
872	L42319	Bos taurus (clone Sal3.8) tristetraprolin	0.007	2507337	TRANSCRIPTION TERMINATION FACTOR RHO	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
873	M59815	Human complement component C4A gene, exons 10 through 41.	0.007	3876769	(Z69637) Similarity to Human Prolyl 4-hydroxylase alpha subunit (SW:P4HA_HUMAN); cDNA EST yk219g12.5 comes from this gene; cDNA EST yk319d8.5 comes from this gene; cDNA EST yk339d11.5 comes from this gene; cDNA EST yk371c9.3...	5.3
874	X63723	B.bovis WC1.1 mRNA	0.007	2969893	(AJ001858) human SIM2 [Homo sapiens]	5.3
875	AB009864	Expression vector pME18S-FL3, complete sequence	0.007	2137618	p45 NF-E2 related factor 2 - mouse musculus]	5.1
876	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	2804497	(AF043705) contains similarity to C2H2-type zinc fingers	5.0
877	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.007	440298	(L27469) product of alternative splicing [Drosophila melanogaster]	4.7
878	X58869	Chicken mRNA for aldehyde dehydrogenase	0.007	1185062	(L75945) flagellar export protein [Borrelia burgdorferi]	4.1
879	AF027735	Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds	0.007	2394390	(AF017434) pmi-like gene product [Methylobacterium extorquens]	4.0
880	AF105228	Bos taurus tuftelin mRNA, complete cds	0.007	3036802	(AL022373) putative protein HYPOTHETICAL 60.2 KD PROTEIN T27F2.1 IN CHROMOSOME V >gi 3880311 gn PID e1349855 BX42 (SW:BX42_DROME); cDNA EST EMBL:C07233 comes from this gene; cDNA EST EMBL:C08532 comes from this gene; cDNA EST yk501h10.3 comes from this gene; cDNA EST yk501f1.3...	3.9
881	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.007	2500814		3.8

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
882	X93567	L.major mRNA for beta-tubulin (1404bp)	0.007	2317862	(U78289) ty lactone synthase modules 4 & 5 [Streptomyces fradiae]	3.0
883	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	3881103	(AL032646) predicted using Genefinder; cDNA EST EMBL:D76407 comes from this gene; cDNA EST EMBL:C08999 comes from this gene; cDNA EST yk199b12.5 comes from this gene; cDNA EST yk282a4.5 comes from this gene; cDNA EST EMBL:CO...	2.7
884	AF041056	Homo sapiens WSCR4 gene, exons 3 and 4	0.007	135817	THROMBIN RECEPTOR PRECURSOR human >gi 339677 (M62424) thrombin receptor [Homo sapiens]	2.2
885	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.007	1723518	HYPOTHETICAL 32.2 KD PROTEIN C22E12.04 IN CHROMOSOME I >gi 1220279 (Z70043) unknown	2.1
886	M74798	Hevea brasiliensis 3-hydroxy-3-methylglutaryl-coenzyme A reductase gene, 3' end.	0.007	1001282	(D64003) polyA polymerase	1.9
887	Z62997	H.sapiens CpG DNA, clone 76g11, reverse read cpg76g11.r1a	0.007	1176532	HYPOTHETICAL 111.9 KD PROTEIN C34E10.8 IN CHROMOSOME III >gi 500731 (U10402) weakly similar to protein C kinase substrate [Caenorhabditis]	1.8
888	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.007	2498317	DVA-1 POLYPROTEIN PRECURSOR nematode polyprotein antigen precursor [Dictyocaulus viviparus] >gi 1585421 prf 2124414A polyprotein antigen/allergen [Dictyocaulus viviparus]	1.2
889	L29426	Synechocystis species (strain PCC 6803) drgA gene, complete cds.	0.007	3882275	(AB018320) KIAA0777 protein [Homo sapiens]	1.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
890	D83329	Mus musculus DNA for prostaglandin D2 synthase, complete cds	0.007	1001741	(D64004) hypothetical protein	0.97
891	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.007	1723928	HYPOTHETICAL 11.6 KD PROTEIN IN NUT1-ARO2 INTERGENIC REGION PRECURSOR YGL149w - yeast (Saccharomyces	0.94
892	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.007	121452	GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR >gi 82606 pir A24266 glutenin high molecular weight chain 12 precursor - wheat >gi 21779	0.79
893	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	0.007	927287	(U30294) ORF2 [Prevotella ruminicola]	0.35
894	Y11918	H.sapiens IMAGE cDNA clone 26881	0.007	1055188	(U40061) contains similarity to transmembrane domains like those found in sugar transporter proteins	0.26
895	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.21
896	L36827	Mus Musculus alphaA-crystallin-binding protein I	0.007	4063019	(AF083061) ABC transporter TliF [Pseudomonas fluorescens]	0.20
897	Z65719	H.sapiens CpG DNA, clone 54c10, reverse read cpg54c10.rt1a.	0.007	1097307	HIC-1 gene [Homo sapiens]	0.20
898	AF064029	Helianthus tuberosus lectin I mRNA, complete cds	0.007	1174915	UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP) >gi 284488 pir S28381 utrophin protein) [Homo sapiens]	0.002
899	AF051730	Mus musculus cathepsin S (CatS) gene, exon 6	0.007	1707017	(U78721) RNA helicase isolog [Arabidopsis thaliana]	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Oryctolagus cuniculus gp42/basigin/OX-47/HT7 mRNA, complete cds.	0.007	2370494	(Z98944) hypothetical protein	2e-04
900	U62398					
901	X76341	M.musculus glutathione reductase mRNA.	0.007	3513303	(AC005594) R26984_1 [Homo sapiens]	8e-07
		Rat (lambda 20B0.5) M-type 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase	0.007	3036809	(AL022373) putative protein (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]	6e-15
902	M26215					
903	AB007902	Homo sapiens KIAA0442 mRNA, partial cds	0.007	2662165		2e-17
		Lactococcus lactis cremoris plasmid pNZ-4000 insertion sequence IS982 putative transposase gene and eps gene cluster (epsRXABCDEFGH IJKL), complete cds	0.007	2731377	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	1e-31
904	U93364					
905	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
		Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
906	AF100694					
907	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
		Arabidopsis thaliana cellulose synthase catalytic subunit (AthB) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
908	AF027174					
909	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.006	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
910	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
911	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
912	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
913	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.006	<NONE>	<NONE>	<NONE>
914	AF064029	Helianthus tuberosus lectin I mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
915	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	<NONE>	<NONE>	<NONE>
916	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.006	4049856	(AF063866) ORF MSV064 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	9.6
917	AF100694	Mus musculus Pontin52 mRNA, complete cds	0.006	3880536	(Z82070) predicted using Genefinder; similar to Lectin C-type domain short and long forms (2 domains); cDNA EST EMBL:C10633 comes from this gene; cDNA EST EMBL:C12424 comes from this gene; cDNA EST yk191e7.3 comes from this ...	7.9
918	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.006	3877761	(Z81552) F56G4.1 [Caenorhabditis elegans] >gi 3878615 gnl PID e1348240 (Z83118) F56G4.1	7.5
919	X80289	H.sapiens PTPL1 mRNA for protein tyrosine phosphatase	0.006	1168791	CATHEPSIN E PRECURSOR precursor - rabbit >gi 402729 (L05418) procathepsin E	7.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
920	AF074386	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	1346371	DIACYLGLYCEROL KINASE, BETA (DIACYLGLYCEROL KINASE) >gi 477059 pir A47744 diacylglycerol kinase (EC 2.7.1.107) beta - rat 90kDa-diacylglycerol kinase [Rattus	5.5
921	U72396	<i>Lycopersicon esculentum</i> class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.006	2196567	(D88588) lipoprotein [Escherichia coli]	4.3
922	AF074387	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	2113798	(Z83259) AmphiBrf38 [Branchiostoma floridae]	4.3
923	AB012106	<i>Brassica rapa</i> mRNA for SRK45, complete cds	0.006	1388166	(U58282) Bowel [Drosophila melanogaster]	4.3
924	AF074386	<i>Sambucus nigra</i> hevein-like protein mRNA, complete cds	0.006	2496785	HYPOTHETICAL 20.1 KD PROTEIN Y4YS	4.2
925	AF012899	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.7
926	AF064029	<i>Helianthus tuberosus</i> lectin 1 mRNA, complete cds	0.006	416592	A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR >gi 101170 pir A41258 a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)	2.5
927	AJ005813	<i>Arabidopsis thaliana</i> mRNA for neoxanthin cleavage enzyme	0.006	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.0
928	U33949	Human Down Syndrome region of chromosome 21, genomic sequence, clone A12H1-1A6.	0.006	3850997	(AF067150) beta-hydroxyacyl-ACP dehydratase precursor	1.9

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1175	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1176	Y09232	H.sapiens fertilin alpha pseudogene	2e-04	<NONE>	<NONE>	<NONE>
1177	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	<NONE>	<NONE>	<NONE>
1178	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1179	AF072847	Homo sapiens putative swelling-activated chloride channel (CLNS1A) gene, intron 6	2e-04	<NONE>	<NONE>	<NONE>
1180	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1181	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	<NONE>	<NONE>	<NONE>
1182	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	1213557	(U50199) coded for by C. elegans cDNA yk89e9.5; coded for by C. elegans cDNA cm7g5; coded for by C. elegans cDNA cm14b9; coded for by C. elegans cDNA yk52g5.5; coded for by C. elegans cDNA yk76e5.5; coded for by C. elegans cDNA yk131f11.5; c...	8.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1183	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	729008	EPITHELIAL DISCOIDIN DOMAIN RECEPTOR I PRECURSOR (TYROSINE- PROTEIN KINASE CAK) (CELL ADHESION KINASE) (TYROSINE KINASE DDR) (DISCOIDIN RECEPTOR TYROSINE KINASE) (TRK E) (PROTEIN-TYROSINE KINASE RTK 6) sapiens]	8.3
1184	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-04	2507582	HYPOTHETICAL 138.1 KD PROTEIN IN MOLR-BGLX INTERGENIC REGION >gi 1788436 (AE000300) putative regulator [Escherichia coli]	7.8
1185	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	2e-04	1085500	collagen alpha 1(EX) chain - mouse musculus] >gi 744962 prf 2015346A collagen:SUBUNIT=alpha1:ISO TYPE=IX [Mus musculus]	7.8
1186	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- A) mRNA, complete cds	2e-04	2623967	(Y13942) GTN Reductase [Agrobacterium radiobacter]	7.4
1187	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	2497316	ADVANCED GLYCOSYLATION END PRODUCT-SPECIFIC RECEPTOR PRECURSOR (RECEPTOR FOR ADVANCED GLYCOSYLATION END PRODUCTS) products receptor precursor - bovine >gi 163651 (M91212) receptor for advanced glycosylation end products [Bos taurus]	5.3
1188	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- B) mRNA, complete cds	2e-04	1001710	(D64004) hypothetical protein	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1189	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	2e-04	3258584	(U41263) The 3' UTR of this gene overlaps the 3' UTR of T19D12.6(confirmed by EST hits) [Caenorhabditis elegans]	2.1
1190	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	2e-04	2736338	(AF038623) contains similarity to RNA recognition motifs	0.89
1191	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	2e-04	2196567	(D88588) lipoprotein [Escherichia coli]	0.69
1192	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	2e-04	3319874	(AJ006096) F-spondin [Branchiostoma floridae]	5e-04
1193	L26049	Chlamydomonas reinhardtii dynein heavy chain alpha (ODA11) gene, exons 2-15, and partial cds.	2e-04	3876775	(Z81077) predicted using Genefinder; Similarity to Yeast protein 8248 (TR:G587531)	2e-09
1194	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1195	AF064029	Helianthus tuberosus lectin 1 mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1196	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	1e-04	<NONE>	<NONE>	<NONE>
1197	X51890	Rhesus monkey interleukin-3 gene	1e-04	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1198	AE001421	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence	1e-04	<NONE>	<NONE>	<NONE>
1199	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	1e-04	<NONE>	<NONE>	<NONE>
1200	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	1e-04	2576287	(Y15086) HepC protein [Cylindrotheca fusiformis]	4.7
1201	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	1e-04	3395673	(AB016623) RWC-3 [Oryza sativa]	0.14
1202	AF038035	Homo sapiens BRCA1-associated RING domain protein (BARD1) gene, exons 2 and 3	9e-05	<NONE>	<NONE>	<NONE>
1203	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	<NONE>	<NONE>	<NONE>
1204	AB012106	Brassica rapa mRNA for SRK45, complete cds	9e-05	<NONE>	<NONE>	<NONE>
1205	U95098	Xenopus laevis mitotic phosphoprotein 44 mRNA, partial cds	9e-05	<NONE>	<NONE>	<NONE>
1206	AF034099	Laccaria bicolor glyoxal malate synthase protein mRNA, complete cds	9e-05	1351553	HYPOTHETICAL LIPOPROTEIN MG348 PRECURSOR >gi 1361668 pir E64238 hypothetical protein MG348 - Mycoplasma genitalium (SGC3) >gi 3844931	8.8

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1207	D50006	Human DNA for alpha-platelet-derived growth factor receptor, exon 6-10	9e-05	3063639	(AF056494) NADH dehydrogenase subunit 5 [Panorpa japonica]	5.1
1208	U50423	Human Down Syndrome region of chromosome 21, clone A41B8-1B7.	9e-05	124273	INHIBIN ALPHA CHAIN PRECURSOR bovine >gi163195 (M13273) inhibin A subunit [Bos taurus]	3.0
1209	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	9e-05	4007782	(X72850) 2,4-dihydroxybenzoate monooxygenase [Sphingomonas sp.]	2.3
1210	AC005276	Homo sapiens clone fragment UWGC:gap3 from 7q31.3, complete sequence [Homo sapiens]	9e-05	1492075	(U60315) MC132L [Molluscum contagiosum virus subtype 1]	1.0
1211	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-05	2887423	(AB007884) KIAA0424 [Homo sapiens]	2e-10
1212	X77772	C.fuscus gamma-M2-1 crystallin mRNA.	9e-05	2072425	(U83115) non-lens beta gamma-crystallin like protein [Homo sapiens]	7e-25
1213	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1214	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1215	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1216	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1217	L06178	Apis mellifera ligustica complete mitochondrial genome	8e-05	<NONE>	<NONE>	<NONE>
1218	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1219	AF100694	Pontin52 mRNA, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1220	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	<NONE>	<NONE>	<NONE>
1221	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	1722841	WNT-11 PROTEIN PRECURSOR (XWNT-11) clawed frog >gi 439108 (L23542) maternal protein	9.9
1222	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1205991	(U35637) nebulin [Homo sapiens]	9.6
1223	AF024605	Homo sapiens serine protease-like protease Sequence 2 from patent US 5736377	8e-05	3242783	(AF055354) respiratory burst oxidase protein B	8.6
1224	Y13148	Rattus norvegicus mRNA for PAC608 gene	8e-05	2314243	(AE000616) alpha-ketoglutarate permease (ketP)	8.1
1225	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	8e-05	1170586	RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1 (P195) (KIAA0051) >gi 627594 pir A54854 Ras GTPase activating-related protein - human sapiens] >gi 536844 (L33075) ras GTPase-activating-like protein [Homo sapiens]	7.8
1226	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	3.5
1227	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	544353	F-SPONDIN PRECURSOR	3.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1228	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-05	483243	apolipoprotein B-100 - chicken (fragment)	3.4
1229	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	91207	proline-rich protein - mouse (fragment) musculus]	2.2
1230	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi1066466	2.2
1231	AF027173	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-A) mRNA, complete cds	8e-05	2499181	ZONADHESIN PRECURSOR >gi1066466	1.9
1232	AB012106	Brassica rapa mRNA for SRK45, complete cds	8e-05	2833647	(AF027972) flagelliform silk protein [Nephila clavipes]	1.6
1233	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	8e-05	1163063	(Z49821) MYO2 [Saccharomyces cerevisiae]	0.90
1234	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	8e-05	1653488	(D90914) hypothetical protein	0.30
1235	M26510	Chicken nonmuscle myosin heavy chain (MHC) gene, complete cds.	8e-05	112159	plectin - rat	0.003
1236	U56402	Human chromatin structural protein homolog	8e-05	2088823	(AF003384) weak similarity to the peptidase family A2	1e-13
1237	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	437181	(U02289) GTPase-activating protein [Caenorhabditis elegans]	2e-17
1238	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-05	465983	HYPOTHETICAL 80.8 KD PROTEIN ZC21.4 IN CHROMOSOME III	8e-27

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1239	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	7e-05	<NONE>	<NONE>	<NONE>
1240	U83656	Rattus norvegicus NF-KB gene, promotor region	7e-05	3880858	(AL031633) predicted using Genefinder; cDNA EST yk304f12.5 comes from this gene [Caenorhabditis elegans]	9.3
1241	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	7e-05	3080538	(AL022600) hypothetical protein	9.2
1242	X89398	H.sapiens ung gene for uracil DNA-glycosylase	7e-05	549700	HYPOTHETICAL 23.7 KD PROTEIN IN MDH1-VMA5 INTERGENIC REGION >gi 539182 pir S37908 hypothetical protein YKL083w - yeast (Saccharomyces cerevisiae) >gi 486120 (Z28082) ORF YKL083w	1.8
1243	M83753	Bovine follicle stimulating hormone-beta subunit gene, complete cds.	7e-05	2398621	(AJ000342) DMBT1 protein, 5.8 kb transcript [Homo sapiens]	1.8
1244	M80829	Rat troponin T cardiac isoform gene, complete cds	5e-05	854065	(X83413) U88 [Human herpesvirus 6]	2e-08
1245	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	4e-05	120240	FLAGELLIN B2 PRECURSOR Methanococcus voltae >gi 150063 (M72148) flagellin	5.2
1246	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1247	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1248	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Rattus norvegicus</i> homer-1c mRNA, complete cds	3e-05	<NONE>	<NONE>	<NONE>
1249	AF093268					
1250	AB012106	<i>Brassica rapa</i> mRNA for SRK45, complete cds	3e-05	2773226	(AF039716) Similar to protein kinase [<i>Caenorhabditis elegans</i>]	6.7
1251	AF100694	<i>Mus musculus</i> Pontin32 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	5.6
1252	U72396	<i>Lycopersicon</i> esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	121855	EXOGLUCANASE II PRECURSOR cellulose 1,4-beta cellobiosidase (EC 3.2.1.91) II precursor - fungus (<i>Trichoderma</i> <i>reesei</i>) 1,4-beta-cellobiosidase (EC 3.2.1.91) II - fungus cellobiohydrolase II [<i>Trichoderma reesei</i>]	4.6
1253	U76524	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	3e-05	3880516	(AL021572) similar to CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE)	3.3
1254	M88299	Mouse brain-1 POU- domain protein, complete cds.	3e-05	1947048	(U66102) intimin [<i>Escherichia</i> <i>coli</i>]	3.0
1255	U95098	<i>Xenopus laevis</i> mitotic phosphoprotein 44 mRNA, partial cds	3e-05	3122872	CELL-CYCLE NUCLEAR AUTOANTIGEN SG2NA (S/G2 NUCLEAR ANTIGEN) >gi 1082650 pir JC2522 nuclear autoantigen - human >gi 805095 (U17989) GS2NA	2.8
1256	U76524	<i>Sambucus nigra</i> ribosome inactivating protein precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - <i>Thermus aquaticus</i> >gi 155083 (M84341) cytochrome c oxidase subunits precursor [<i>Thermus</i> <i>thermophilus</i>]	2.6
1257	U72396	<i>Lycopersicon</i> esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	3e-05	2811015	SEGMENTATION POLARITY PROTEIN ENGRAILED >gi 2076747 (U42429) engrailed [<i>Anopheles gambiae</i>] >gi 2148918 (U42214) engrailed [<i>Anopheles gambiae</i>]	2.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1258	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-05	1657752	(U62325) FE65-like protein [Homo sapiens]	1.7
1259	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-05	2072961	(U93568) putative p150 [Homo sapiens]	1.5
1260	U76523	Sambucus nigra lectin precursor mRNA, complete cds	3e-05	1352145	CYTOCHROME C OXIDASE POLYPEPTIDE I chain I - Thermus aquaticus >gi 155083 (M84341) cytochrome c oxidase subunits precursor [Thermus thermophilus]	1.1
1261	X91890	H.sapiens regulatory region of HOXA7 gene	3e-05	111013	Sxr (Bkm-homolog) sex-determining region protein - mouse	1.0
1262	L36936	Homo sapiens metase gene, partial cds.	3e-05	1944352	(D84239) IgG Fe binding protein [Homo sapiens]	0.99
1263	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	417782	SMP2 PROTEIN >gi 320853 pir S30911 SMP2 protein - yeast (Saccharomyces cerevisiae) gene [Saccharomyces cerevisiae]	0.89
1264	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-05	1708501	INTEGRIN ALPHA CHAIN-LIKE PROTEIN alpha Int1p [Candida albicans]	0.39
1265	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-05	1587031	cis-Golgi matrix protein GM130 [Rattus norvegicus]	0.20
1266	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-05	2072964	(U93569) putative p150 [Homo sapiens]	0.049

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1267	Z96668	H.sapiens telomeric DNA sequence, clone 7PTELO01, read 7PTELOO001.seq	3e-05	542429	glycosylated and mynstitlated smaller surface antigen - Plasmodium falciparum >gi 836640 (X76298) glycosylated and myristilated smaller surface antigen gallus] >gi 1092178 prf 2023165B surface antigen	0.029
1268	AB012105	Brassica rapa mRNA for SLG45, complete cds	3e-05	3879121	(Z70310) predicted using Genefinder: Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES... Genefinder; Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL:T01923 comes from this gene; cDNA EST EMBL:D32335 comes from this gene; cDNA EST EMBL:D32723 comes from this gene; cDNA ES...	2e-13
1269	AF074385	Sambucus nigra hevein-like protein mRNA, complete cds	3e-05	2497677	ZYXIN (ZYXIN 2) sapiens] >gi 1545954 gn PID e223417 (X95733) zyxin	2e-23
1270	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath- B) mRNA, complete cds	1e-05	<NONE>	<NONE>	<NONE>
1271	X16318	Canine mRNA for signal recognition particle 54k protein	1e-05	3122612	PITUITARY HOMEBOX 3 (HOMEBOX PROTEIN PITX3) >gi 2645427 (AF005772) homeobox protein Pitx3 [Mus musculus]	4.4
1272	AB012105	Brassica rapa mRNA for SLG45, complete cds	1e-05	1652458	(D90905) DNA mismatch repair protein MutL [Synechocystis sp.]	0.62

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1273	U57843	Human phosphatidylinositol 3-kinase delta catalytic subunit mRNA, complete cds	1e-05	475909	(X67098) ORF1A [Homo sapiens]	0.22
1274	Z96569	H.sapiens telomeric DNA sequence, clone 2QTELO54, read 2QTELOO054.seq	1e-05	2137043	unknown protein - rabbit (fragment) cuniculus]	0.005
1275	AE000810	Methanobacterium thermoautotrophicum from bases 172512 to 182957 (section 16 of 148) of the complete genome	1e-05	3877579	(E02271) similarity to mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes... Mouse kinensin-like protein KIF4 (SW:P33174); cDNA EST EMBL:D27320 comes from this gene; cDNA EST EMBL:D27322 comes from this gene; cDNA EST EMBL:D27321 comes from this gene; cDNA EST EMBL:D35764 comes...	6e-27
1276	AB012113	Homo sapiens gene for CC chemokine PARC precursor, complete cds	9e-06	<NONE>	<NONE>	<NONE>
1277	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-52411 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	9e-06	<NONE>	<NONE>	<NONE>
1278	D86245	Human MHC (HLA) DRB intron 1 DNA, partial sequence	9e-06	1051253	(U37531) mucin apoprotein [Mus musculus]	1.3
1279	D79998	Human mRNA for KIAA0176 gene, partial cds	9e-06	2833253	HYPOTHETICAL PROTEIN KIAA0176 sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1280	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-33
1281	U10246	Toxoplasma gondii RH uracil phosphoribosyl transferase gene, complete cds.	9e-06	3876090	(Z69635) Similarity to Yeast uridine kinase (SW:URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this ge...	7e-34
1282	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1283	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-06	<NONE>	<NONE>	<NONE>
1284	U66340	Human Rh blood group C antigen (RHCE) gene, exon 2, partial cds	8e-06	1707155	(U80837) F07E5.6 gene product [Caenorhabditis elegans]	9.6
1285	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-06	<NONE>	<NONE>	<NONE>
1286	M29930	Human insulin receptor (allele 2) gene, exons 14, 15, 16 and 17.	4e-06	<NONE>	<NONE>	<NONE>
1287	L42103	Homo sapiens (subclone 5_d3 from P1 H25) DNA sequence.	3e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1288	AF012244	cerberus-like (Cer-1) gene, complete cds	3e-06	<NONE>	<NONE>	<NONE>
1289	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1290	Z69366	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST.	3e-06	<NONE>	<NONE>	<NONE>
1291	X85232	H.sapiens chromosome 3 sequences	3e-06	<NONE>	<NONE>	<NONE>
1292	M32674	Human platelet glycoprotein IIIa, exons 7, 8 and 9.	3e-06	<NONE>	<NONE>	<NONE>
1293	D16879	Human HepG2 3' region cDNA, clone hmd2a01	3e-06	998296	(U33484) ependymin [Hemiodus sp.]	5.6
1294	U18614	Lagothrix lagotricha interphotoreceptor retinoid-binding protein (IRBP) gene, intron 1, complete sequence	3e-06	1613846	(U71440) polyprotein [Rice tungro spherical virus]	5.0
1295	AF090115	Lycopersicon esculentum cytosolic class II small heat shock protein HCT2 (HSP17.4) mRNA, complete cds	3e-06	1477646	(U53204) plectin [Homo sapiens] >gi1477651 (U63610) plectin [Homo sapiens]	4.0
1296	AF016898	Homo sapiens B-ATF gene, complete cds	3e-06	1085177	reverse transcriptase - fruit fly reverse transcriptase [Drosophila yakuba]	3.0
1297	AB018490	Homo sapiens DNA, trinucleotide repeats region	3e-06	3876572	(Z81522) predicted using Genefinder; similar to RNA recognition motif. (aka RRM, RBD, or RNP domain) [Caenorhabditis elegans]	3.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1298	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	3e-06	4240137	(AB020631) KIAA0824 protein [Homo sapiens]	2.7
1299	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1300	M37929	Homo sapiens adenosine monophosphate deaminase 1 (AMPD1) gene, exons 11-12.	3e-06	1653775	(D90916) thiol:disulfide interchange protein DsbD [Synechocystis sp.]	1.7
1301	U60496	Glycine max actin (Soy86) gene, partial cds	3e-06	1730738	ACTIN-LIKE PROTEIN ARP5 Ynl2430p [Saccharomyces cerevisiae]	2e-05
1302	X14363	Yersinia pseudotuberculosis rplC, rplD, rplW, rplB and rpsS genes for ribosomal proteins L3, L4, L23, L2 and S19	3e-06	585879	50S RIBOSOMAL PROTEIN L2 maritima >gij437926 (Z21677) ribosomal protein L2	2e-12
1303	Z34969	H.sapiens DNA for microsatellite polymorphism	2e-06	<NONE>	<NONE>	<NONE>
1304	X64707	H.sapiens BBC1 mRNA	1e-06	<NONE>	<NONE>	<NONE>
1305	AC005830	Homo sapiens Xp22-154-155 BAC GSHB-524I1 (Genome Systems Human BAC Library), complete sequence [Homo sapiens]	1e-06	<NONE>	<NONE>	<NONE>
1306	J04058	Human electron transfer flavoprotein alpha-subunit mRNA, complete cds.	1e-06	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1307	L25647	Homo sapiens fibroblast growth factor receptor gene (located in the central MHC) signal peptide and consecutive exon	1e-06	1586734	mxoQ gene [Methylobacterium organophilum] (U20633) NADH dehydrogenase subunit [Neuwiedia veratrifolia]	5.4
1308	L26261	Human MHC class III HLA-RP1 gene.	1e-06	1684985		1.8
1309	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	1e-06	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-17
1310	M10935	Human haptoglobin gene (alpha-2 allele), complete cds and haptoglobin-related gene, exon 1 and three Alu repeats.	6e-07	<NONE>	<NONE>	<NONE>
1311	AC002251	Homo sapiens (subclone 1_g6 from BAC H76) DNA sequence	4e-07	2144491	coagulation factor Xa (EC 3.4.21.6) precursor norvegicus]	4.2
1312	AF047717	Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds	4e-07	699196	(U15181) 4-coumarate-coA ligase [Mycobacterium leprae]	1e-06
1313	U14417	Human Ral guanine nucleotide dissociation stimulator mRNA, partial cds.	4e-07	544402	GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) >gi 321257 pir S28415 guanine nucleotide dissociation stimulator ralGDS - mouse >gi 193573 L07924) guanine nucleotide dissociation stimulator [Mus musculus]	8e-08
1314	Z79027	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20G8	3e-07	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1315	U67167	Homo sapiens intestinal mucin (MUC2) gene, promoter region and partial cds	3e-07	<NONE>	<NONE>	<NONE>
1316	AF086256	Homo sapiens full length insert cDNA clone ZD41C11	3e-07	<NONE>	<NONE>	<NONE>
1317	U67228	Human clone HS4.61 Alu-Ya5 sequence	3e-07	1938437	(U97003) contains similarity to C4-type zinc fingers and a ligand-binding domain of nuclear hormone receptors	2.3
1318	U94346	Human calpain-like protease (hura-3) mRNA, complete cds	3e-07	2911858	(AF047659) No definition line found [Caenorhabditis elegans]	0.39
1319	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	1e-07	<NONE>	<NONE>	<NONE>
1320	X13596	Bean DNA for glycine-rich cell wall protein GRP 1.8	1e-07	<NONE>	<NONE>	<NONE>
1321	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rhoh12 gene, 3' end.	1e-07	1326385	(U58751) C07G1.7 gene product [Caenorhabditis elegans]	8.0
1322	Z55905	H.sapiens CpG DNA, clone 71f4, forward read cpg71f4.ft1a.	1e-07	1076802	extensin-like protein - maize >gi 600118 mays]	0.61
1323	X03541	Human mRNA of trk oncogene > :: gb J96186 J96186 Sequence 23 from patent US 5734039	1e-07	325465	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1324	AF027766	Canis familiaris Y-linked zinc finger protein	1e-07	220643	(D10628) zinc finger protein [Mus musculus]	7e-08
1325	D13613	Bovine mRNA for rabphilin-3A, complete cds > :: dbj E07809 E07809 cDNA encoding rabphilin-3A	1e-07	2822161	(AC004082) rab3 effector-like; 35% Similarity to AF007836 (PID:g2317778) [Homo sapiens]	6e-11

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1326	X57110	Human mRNA for c-cbl proto-oncogene	1e-07	323270	(J04169) gag-onc fusion protein [Cas NSI retrovirus]	3e-14
1327	X57110	Human mRNA for c-cbl proto-oncogene	1e-07	115855	PROTO-ONCOGENE C-CBL human >gi 29731 (X57110) c-cbl protein [Homo sapiens]	4e-19
1328	AC001178	Homo sapiens (subclone 2_g12 from BAC H94) DNA sequence	4e-08	<NONE>	<NONE>	<NONE>
1329	U11866	Human interleukin-8 receptor type B (IL8RB) gene, promoter and exons 1-6	4e-08	<NONE>	<NONE>	<NONE>
1330	AC001225	Homo sapiens (subclone 2_e6 from BAC H94) DNA sequence	4e-08	478184	histone H1 II-1 (clone L95) - midge	6.5
1331	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	4e-08	141448	HYPOTHETICAL 32.6 KD PROTEIN IN TRANSPOSON TN4556 >gi 80758 pir JQ0428 hypothetical 32.6K protein - Streptomyces fradiae transposon Tn4556	4.7
1332	AC006164	Homo sapiens clone UWGC:y28gap from 6p21, complete sequence [Homo sapiens]	4e-08	2580578	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens]	1.2
1333	X01060	Human mRNA for transferrin receptor	4e-08	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.61
1334	Y10697	H.sapiens INE2 mRNA	4e-08	124909	INSULIN RECEPTOR-RELATED PROTEIN PRECURSOR (IRR) (IR-RELATED RECEPTOR) >gi 186555 sapiens]	0.14
1335	U60416	Rattus norvegicus myr 6 myosin heavy chain mRNA, complete cds	4e-08	102189	myosin I, high molecular weight - Acanthamoeba sp	3e-08

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1336	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	4e-08	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-28
1337	AE000213	Escherichia coli K-12 MG1655 section 103 of 400 of the complete genome	4e-08	3294172	(AL022325) tF27C3.1.1 (protein similar to C. elegans protein B0035.16) (isoform 1) [Homo sapiens]	2e-67
1338	D89821	Mus musculus mRNA for RhoM, complete cds	2e-08	3024539	RHO-RELATED GTP-BINDING PROTEIN RHOD (RHO-RELATED PROTEIN HP1) (RHOHP1) sapiens]	1e-04
1339	U74382	Human telomeric repeat DNA-binding protein (PIN2) mRNA, complete cds	1e-08	<NONE>	<NONE>	<NONE>
1340	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	1e-08	<NONE>	<NONE>	<NONE>
1341	L21936	Human succinate dehydrogenase flavoprotein subunit	1e-08	3201678	(AF060886) adenine phosphoribosyltransferase [Leishmania tarentolae]	4.0
1342	AB009777	Homo sapiens gene for osteonidogen, promoter region	1e-08	479388	tritin - wheat >gi 391929 gnl PID d1003454	2.2
1343	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.9
1344	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	1e-08	1730173	GLUCOSE-6-PHOSPHATE ISOMERASE, CYTOSOLIC 2 (GPI) (PHOSPHOGLUCOSE ISOMERASE) (PGI) isomerase [Clarkia concinna]	1.7
1345	AC000980	Homo sapiens (subclone 1_g2 from P1 H31) DNA sequence	1e-08	439877	(L27423) reverse transcriptase [Homo sapiens]	1.1

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1346	U48734	Human non-muscle alpha-actinin mRNA, complete cds	1e-08	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.19
1347	M76724	Human leukocyte adhesion receptor alpha subunit	1e-08	1177607	(X92485) pval [Plasmodium vivax]	0.19
1348	AF067959	Gallus gallus homeodomain protein HOXD-3 mRNA, complete cds	1e-08	3165574	(AF067942) No definition line found [Caenorhabditis elegans]	0.15
1349	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	1e-08	2072964	(U93569) putative p150 [Homo sapiens]	0.001
1350	X57103	Human h-lys gene for lysozyme (upstream region)	7e-09	<NONE>	<NONE>	<NONE>
1351	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	7e-09	231629	BILE-SALT-ACTIVATED LIPASE PRECURSOR ESTER LIPASE) (STEROL ESTERASE) (CHOLESTEROL ESTERASE) salt-activated lipase [Homo sapiens] sapiens]	0.22
1352	L34741	Aplysia californica prohormone convertase (PC2) mRNA, complete cds.	5e-09	322054	cytochrome-c oxidase (EC 1.9.3.1) chain II precursor - Synechocystis sp. (PCC 6803) >gi 581739 sp.]	5.0
1353	AF052959	Homo sapiens type XV collagen (COL15A1) gene, exon 6	4e-09	131269	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72708 pir QJL V6A photosystem II chlorophyll a-binding protein psbB - liverwort (Marchantia polymorpha) chloroplast >gi 11700	1.8

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1354	L15470	Streptomyces clavuligerus (NRRL 3585) clavulanic acid biosynthesis protein (cla) gene, complete cds and clavamate synthase 2 (cs2) gene, partial cds.	4e-09	586028	PROCLAVAMINIC ACID AMIDINO HYDROLASE (AUH) (PROCLAVAMINIC ACID AMIDINO HYDROLASE) >gi 1361423 pir S57669 Proclavaminic acid amidino hydrolase - Streptomyces clavuligerus >gi 295171 Proclavaminic acid amidino hydrolase [Streptomyces clavuligerus] >gi 1586122 prf 2203286B proclavaminic acid amidino hydrolase [Streptomyces clavuligerus]	4e-13
1355	AB002302	Human mRNA for KIAA0304 gene, complete cds	2e-09	131600	GENERAL SECRETION PATHWAY PROTEIN L product [Klebsiella pneumoniae] >gi 149311 (M32613) pulL	2.5
1356	L34219	Homo sapiens retinaldehyde-binding protein (RALBP) gene, complete cds.	1e-09	<NONE>	<NONE>	<NONE>
1357	AB002302	Human mRNA for KIAA0304 gene, complete cds	1e-09	2224549	(AB002302) KIAA0304 [Homo sapiens]	5.0
1358	D85731	Homo sapiens HSPA1L gene for Heat shock protein 70 testis variant, 5'UTR, partial sequence	1e-09	1389766	(U58658) unknown [Homo sapiens]	1.3
1359	AF064483	Homo sapiens natural resistance-associated macrophage protein 2 (NRAMP2) gene, exon 17, alternatively spliced non-IRE form, complete cds	8e-10	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.72

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1360	AF002283	Mus musculus alpha-actinin-2 associated LIM protein mRNA, alternatively spliced product, complete cds	6e-10	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-21
1361	M26220	African green monkey origin of replication	5e-10	2143455	gene DMR-N9 protein - mouse (fragment)	8.8
1362	Z78006	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA7F10	4e-10	2072977	(U93574) putative p150 [Homo sapiens]	0.005
1363	U82303	Homo sapiens unknown protein mRNA, partial cds	2e-10	1825711	(U88183) similar to the immunoglobulin superfamily, most similar to neural cell adhesion proteins [Caenorhabditis elegans]	0.031
1364	AF079764	Drosophila melanogaster enhancer of polycomb	2e-10	3757890	(AF079764) enhancer of polycomb [Drosophila melanogaster]	1e-10
1365	L24123	Homo sapiens NRF1 protein (NRF1) mRNA.	2e-10	3004573	(AC004520) similar to NFE2-related transcription factors; similar to [48694 (PID:g2137676) [Homo sapiens]	4e-53
1366	M91454	Orangutan alpha-globin gene duplicate region.	1e-10	464239	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 1085185 pir S52968 NADH dehydrogenase chain 4 - honeybee mitochondrion (SGC4) >gi 552446 (L06178) NADH dehydrogenase subunit 4 [Apis mellifera ligustica]	6.0
1367	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	6e-11	473912	(L31961) phosphoprotein [Mus cookii]	2.2
1368	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1369	AC001002	(subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1370	AB007874	Homo sapiens KIAA0414 mRNA, partial cds	5e-11	<NONE>	<NONE>	<NONE>
1371	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1372	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1373	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1374	AC001002	Homo sapiens (subclone 2_h9 from P1 H39) DNA sequence	5e-11	<NONE>	<NONE>	<NONE>
1375	Z21852	H.sapiens mRNA for HERV-K long terminal repeat	5e-11	419481	gag polyprotein - human endogenous virus S71	4.6
1376	AB007928	Homo sapiens mRNA for KIAA0459 protein, partial cds	5e-11	2947238	(AF051782) diaphanous 1 [Homo sapiens]	2.8
1377	D87117	House mouse; Musculus domesticus brain mRNA for SAP102, complete cds	5e-11	473912	(L31961) phosphoprotein [Mus cookii]	1.8
1378	AJ131501	Homo Sapiens DNA sequence between two AML1 gene promoters, 6423 BP	5e-11	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.20
1379	M27826	Human endogenous retroviral protease mRNA, complete cds.	5e-11	88558	retroviral proteinase-like protein - human	0.002

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 55.2 KD	
1380	U23804	Drosophila melanogaster putative GTP-binding regulatory protein beta chain (GPB) mRNA, partial cds.	5e-11	2494916	TRP-ASP REPEATS CONTAINING PROTEIN T10F2.4 IN CHROMOSOME III protein; similar to G-Beta repeat region (Trp-Asp domains) of guanine nucleotide binding protein	1e-30
1381	Z22784	M.musculus troponin I gene.	3e-11	3892202	(AF072889) transcription repressor brain factor 2	0.053
1382	AB007880	Homo sapiens KIAA0420 mRNA, complete cds	2e-11	<NONE>	<NONE>	<NONE>
1383	AF020361	9 Homo sapiens BAX gene, exon 6, partial sequence	2e-11	<NONE>	<NONE>	<NONE>
1384	L35600	Homo sapiens DNA sequence.	2e-11	1174952	GLYCOPROTEIN D PRECURSOR gD [Bovine herpesvirus 1]	0.25
1385	U21943	Human organic anion transporting polypeptide	2e-11	2738223	(U95011) brain-specific organic anion transporter	9e-19
1386	U90878	Homo sapiens carboxyl terminal LIM domain protein	2e-11	2996196	(AF053367) carboxyl terminal LIM domain protein [Mus musculus]	4e-23
1387	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	6e-12	<NONE>	<NONE>	<NONE>
1388	M25828	Human von Willebrand factor gene, exon 1, 2, and 3, and three Alu repetitive elements.	6e-12	<NONE>	<NONE>	<NONE>
1389	AB020648	Homo sapiens mRNA for KIAA0841 protein, partial cds	3e-12	<NONE>	<NONE>	<NONE>
1390	Z15026	H.sapiens genes for tumor necrosis factor (Tnfa) and lymphotoxine (Tnfb)	2e-12	<NONE>	<NONE>	<NONE>
1391	L28101	Homo sapiens kallistatin (PI4) gene, exons 1-4, complete cds	2e-12	<NONE>	<NONE>	<NONE>
1392	Z47046	Human cosmid QLL2C9 from Xq28	2e-12	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA20E2	2e-12	106322	hypothetical protein (L1H 3' region) - human	1.5
1393	Z79007	Human tyrosine kinase TXK (txk) gene, exon 13.	1e-12	151484	(M55524) ORF 4; putative [Pseudomonas aeruginosa]	4.3
1394	U34377	Mus musculus app-1 gene for novel member of heat shock protein 110, promoter region	1e-12	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.5
1395	D70845	Human vascular endothelial growth factor gene, exon 8.	1e-12	3982737	(AF069731) calmodulin-dependent protein kinase II beta M isoform [Rattus norvegicus]	0.083
1396	M63978	Homo sapiens lysosomal alpha-mannosidase (manB) mRNA, complete cds	8e-13	<NONE>	<NONE>	<NONE>
1397	U60266	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	5e-34
1398	Z68297	Caenorhabditis elegans cosmid F11A10, complete sequence [Caenorhabditis elegans]	7e-13	2393734	(AC002542) similar to C. elegans F11A10.5; 80% similarity to Z68297 (PID:g1130619) [Homo sapiens]	3e-38
1399	Z68297	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.	6e-13	<NONE>	<NONE>	<NONE>
1400	Z68885	H.sapiens DAP-kinase mRNA	6e-13	2911154	(AB007143) ZIP-kinase [Mus musculus]	0.007
1401	X76104	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA13G4	5e-13	106322	hypothetical protein (L1H 3' region) - human	2e-06
1402	Z78668	Homo sapiens DNA sequence.	3e-13	3184290	(AC004136) hypothetical protein [Arabidopsis thaliana]	1.7
1403	L35600					

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Cloning vector				
1404	AF090452	pKODT complete sequence	2e-13	3876730	(Z49966) F35C11.4 [Caenorhabditis elegans]	7.8
1405	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	2e-13	419481	gag polyprotein - human endogenous virus S71	3.4
1406	AF005219	Homo sapiens transcription factor HOXD13	2e-13	2822166	(AC004080) transcription factor HOXA13 [Homo sapiens]	5e-09
1407	AB018301	Homo sapiens mRNA for KIAA0758 protein, partial cds	2e-13	3882237	(AB018301) KIAA0758 protein [Homo sapiens]	1e-23
1408	D70845	Mus musculus apg-1 gene for novel member of heat shock protein 110, promoter region	1e-13	113658	ALKALINE PROTEINASE PRECURSOR (ALP) precursor - fungus (Acremonium chrysogenum)	3.1
1409	AG000691	Homo sapiens genomic DNA, 21q region, clone: T171BG33	8e-14	930045	(X15332) alpha-1 (III) collagen [Homo sapiens]	3e-04
1410	D30785	Mouse mRNA for neuropsin, complete cds	8e-14	3559978	(AJ005641) serine protease [Rattus rattus]	2e-12
1411	U32710	Haemophilus influenzae Rd section 25 of 163 of the complete genome	8e-14	4106673	(AL035064) queuine trna-ribosyltransferase [Schizosaccharomyces pombe]	2e-38
1412	AG000886	Homo sapiens genomic DNA, 21q region, clone: 64E11X19	7e-14	1363925	hypothetical protein 2 - North American opossum (fragment) >gi 897721 (Z48955) ORF-2, putative RT [Didelphis virginiana]	1.1
1413	Z62664	H.sapiens CpG DNA, clone 71d11, forward read cpg71d11.ft1a.	7e-14	3953461	(AC002328) F20N2.6 [Arabidopsis thaliana]	0.085
1414	AB014532	Homo sapiens mRNA for KIAA0632 protein, partial cds	7e-14	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.040

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1415	Z96478	H.sapiens telomeric DNA sequence, clone 20PTELO04, read 20PTELOO004.seq	7e-14	2981631	(AB012223) ORF2 [Canis familiaris]	2e-04
1416	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1417	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	4e-14	<NONE>	<NONE>	<NONE>
1418	AF033349	Homo sapiens MLL gene breakpoint cluster region, intron 1, partial sequence	3e-14	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	9.3
1419	AC001526	Homo sapiens (subclone 4_f6 from P1 H54) DNA sequence	3e-14	99861	extensin - almond >gi 20420 (X65718) extensin	9.2
1420	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-14	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.15
1421	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-14	3913573	EPHRIN-A2 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 6) (LERK-6) sapiens] >gi 2924761 (AC004258) EPL6_HUMAN [Homo sapiens] E1B PROTEIN, SMALL T-ANTIGEN (E1B 19K) >gi 74142 pir Q1AD25 early E1B 21K protein II - human adenovirus 5 >gi 58489 (X02996) mRNA 5 first reading frame [Human adenovirus type 5] adenovirus type 5] >gi 209797 (J01969) 21 kD protein	8.7
1422	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-15	119040		1.5

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					transcription factor GATA-4,	
1423	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-15	477102	retinoic acid-inducible - mouse >gi 293345 (M98339) GATA-binding transcription factor [Mus musculus]	0.57
1424	AB012223	Canis familiaris LINE 1 element ORF2 mRNA, complete cds	8e-15	92385	hypothetical protein - rat (fragment)	0.003
1425	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-15	<NONE>	<NONE>	<NONE>
1426	X12433	Human pHS1-2 mRNA with ORF homologous to membrane receptor proteins	3e-15	422532	collagen alpha 3(IV) chain - sea urchin	8.9
1427	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-15	1353143	PROBABLE NUCLEAR HORMONE RECEPTOR E02H1.7 >gi 3875431 gnl PID e1344980 (Z47075) similar to Zinc finger, C4 type (two domains) [Caenorhabditis elegans]	5.0
1428	Z69651	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	3e-15	403460	(L24521) transformation-related protein [Homo sapiens]	0.60
1429	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-15	108750	Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine >gi 440 (X62916) anti-testosterone antibody [Bos taurus]	1.1
1430	X83299	H.sapiens SMA3 mRNA	2e-15	671530	(X83299) SMA3 gene product [Homo sapiens]	0.32
1431	U01877	Human p300 protein mRNA, complete cds. >:: gb I62297 I62297 Sequence 1 from patent US 5658784	2e-15	3024341	E1A-ASSOCIATED PROTEIN P300	0.019

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1432	X16516	Mouse MHC (Qa) Q2k gene for class I antigen. exons 4-8	1e-15	2496897	HYPOTHETICAL 45.1 KD PROTEIN CT16C10.6 IN CHROMOSOME III >gi 3874384 gnl PID e1344078 EST EMBL:C08256 comes from this gene; cDNA EST EMBL:C09941 comes from this gene; cDNA EST yk340a10.3 comes from this gene; cDNA EST yk340a10.5 comes from this gene [Ca...	7e-08
1433	M74165	Chicken tensin mRNA, complete cds.	1e-15	283920	tensin - chicken >gi 212752 (M74165) tensin	2e-19
1434	X71893	H.sapiens gene for immunoglobulin kappa light chain variable region O4 and O5	9e-16	<NONE>	<NONE>	<NONE>
1435	U05227	Human Rar protein mRNA, complete cds.	9e-16	3036779	(284479) match: multiple proteins; match: O00407 Q12829 P22127 P36861 Q40219; match: P70550 Q41022 P22125 Q08153 P35286; match: P51148 P51147 P35293 P36861 P35289; match: P35284 Q40217 P51152 P51157 P51158; match: Q41022	3e-06
1436	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	9e-16	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-28
1437	X16145	Rat mRNA for liver alpha-L-Fucosidase (EC 3.2.1.51)	9e-16	67502	alpha-L-fucosidase (EC 3.2.1.51) precursor, tissue - human >gi 178409 (M29877) alpha-L-fucosidase precursor (EC 3.2.1.5) [Homo sapiens]	2e-29
1438	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-16	<NONE>	<NONE>	<NONE>
1439	AF076981	Mus musculus brain mitochondrial carrier protein BMCPI (Bmcpl) mRNA, complete cds	8e-16	3851540	(AF078544) brain mitochondrial carrier protein-1 [Homo sapiens]	2e-13

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens MN/CA9			!!!! ALU SUBFAMILY J	
1440	Z54349	GENE	5e-16	728831	WARNING ENTRY	0.002
1441	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	3e-16	309123	(M35526) complement component C5D [Mus musculus]	3.1
1442	X64587	M.musculus mRNA for splicing factor U2AF (65 kD)	3e-16	2143767	glycoprotein - rat >gi 986943 (L08134) glycoprotein [Rattus norvegicus] norvegicus]	0.003
1443	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	3e-16	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-20
1444	Z73987	Human DNA sequence from cosmid N120B6 on chromosome 22 Contains ESTs, complete sequence [Homo sapiens]	1e-16	<NONE>	<NONE>	<NONE>
1445	M58318	Homo sapiens ala gene.	1e-16	<NONE>	<NONE>	<NONE>
1446	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-16	1552584	(Z80233) hypothetical protein Rv0029	1.3
1447	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	9e-17	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	2e-20
1448	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-17	<NONE>	<NONE>	<NONE>
1449	M76762	Mus musculus ribosomal protein (Kc3) gene, exons 1 to 5, and complete cds.	1e-17	1073048	pupR protein - Pseudomonas putida >gi 525260	0.36
1450	D50561	Human DNA, replication enhancing element (REE1)	4e-18	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.78
1451	D16431	Human mRNA for hepatoma-derived growth factor, complete cds	4e-18	3242079	(AJ006984) proline-rich protein	0.018

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1452	AF088983	Mus musculus heat shock protein hsp40-3 mRNA, complete cds	4e-18	3873707	(Z73102) Similarity to B.subtilis DNAJ protein (SW:DNAJ_BACSU); cDNA EST yk437a1.5 comes from this gene [Caenorhabditis elegans]	9e-25
1453	U60205	Human methyl sterol oxidase (ERG25) mRNA, complete cds	3e-18	<NONE>	<NONE>	<NONE>
1454	AF038177	Homo sapiens clone 23899 mRNA sequence	1e-18	1360775	G protein-coupled receptor 74 - equine herpesvirus 2 >gi 695246 (U20824) G protein-coupled receptor [Equine herpesvirus 2]	5.1
1455	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-21
1456	AB014561	Homo sapiens mRNA for KIAA0661 protein, complete cds	1e-18	3327136	(AB014561) KIAA0661 protein [Homo sapiens]	1e-22
1457	U34374	Human tyrosine kinase TXK (txk) gene, exons 9 and 10.	1e-19	<NONE>	<NONE>	<NONE>
1458	AB006969	Homo sapiens hGAA1 mRNA, complete cds	1e-19	4151809	(AF102855) synaptic SAPAP-interacting protein Synamon	0.19
1459	AB002293	Human mRNA for KIAA0295 gene, partial cds	1e-19	2224531	(AB002293) KIAA0295 [Homo sapiens]	6e-17
1460	Z59664	H.sapiens CpG DNA, clone 168f9, reverse read cpg168f9.rtl.a.	5e-20	3880251	(Z82055) predicted using Genefinder	6.5
1461	M73837	Human modulator recognition factor 2 (MRF-2) mRNA, complete cds.	5e-20	284313	modulator recognition factor 2 - human factor 2 [Homo sapiens]	0.019

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1462	U24267	Human pyrroline-5-carboxylate dehydrogenase	5e-20	2506350	DELTA1-PYRROLINE-5-CARBOXYLATE DEHYDROGENASE PRECURSOR (P5C DEHYDROGENASE) >gi 1353248 sapiens] >gi 1353250 (U24267) pyrroline 5-carboxylate dehydrogenase [Homo sapiens] >gi 1589585 prf 2211355A Delta1-pyrroline-5-carboxylate dehydrogenase [Homo sapiens]	5e-04
1463	U13262	Mus musculus myelin gene expression factor	4e-20	536926	(U13262) myelin gene expression factor [Mus musculus]	3e-07
1464	U13262	Mus musculus myelin gene expression factor	4e-20	3126878	(AF061832) M4 protein deletion mutant [Homo sapiens]	1e-08
1465	Z61239	H.sapiens CpG DNA, clone 48f10, forward read cpg48f10.ft1a.	4e-20	1669601	(D88747) AR401 [Arabidopsis thaliana]	8e-19
1466	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	1e-20	3462455	(U89915) junctional adhesion molecule [Mus musculus]	7e-11
1467	AF029071	Gallus gallus p52 pro-apototic protein mRNA, complete cds	7e-22	2599492	(AF029071) p52 pro-apototic protein [Gallus gallus]	1e-15
1468	M25636	Figure 4. Nucleotide sequence of the pKS36 1.797 kb insert.	6e-22	1196398	(M21305) unknown protein [Homo sapiens]	0.65
1469	AB020655	Homo sapiens mRNA for KIAA0848 protein, complete cds	6e-22	4240325	(AB020725) KIAA0918 protein [Homo sapiens]	1e-19

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1470	S80935	chorionic gonadotropin beta 1 (CG beta 1) subunit	5e-22	115310	PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR >gi 84917 pir A31893 collagen alpha 1(IV) chain precursor - fruit fly (Drosophila melanogaster) melanogaster] >gi 157078 (M96575) type IV collagen pro-collagen [Drosophila melanogaster]	0.027
1471	AF053066	Homo sapiens microsatellite D5S2926 sequence	2e-22	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-04
1472	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	2e-22	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z [Danio rerio]	5e-14
1473	AF064250	Gallus gallus ubiquitin specific protease 66	2e-22	2736064	(AF016107) ubiquitin specific protease 41 [Gallus gallus]	7e-37
1474	AF030880	Homo sapiens pendrin (PDS) mRNA, complete cds	2e-22	729367	DRA PROTEIN (DOWN-REGULATED IN ADENOMA) >gi 2135020 pir A47456 down-regulated in adenoma (DRA) - human >gi 291964 (L02785) Nuclear localization signal at AA 569-573, 576-580, 579-583; acidic transer. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens]	4e-53
1475	AF100694	Mus musculus Pontin52 mRNA, complete cds	6e-23	<NONE>	<NONE>	<NONE>
1476	X57398	Human mRNA for pM5 protein	3e-23	107350	Pm5 protein - human >gi 1335273 gnl PIDe36241	1e-04
1477	AB010998	Rattus norvegicus PAD-R11 mRNA for Peptidylarginine deiminase type I, complete cds	2e-23	<NONE>	<NONE>	<NONE>
1478	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	9.8
1479	D10871	Human h NAT allele 2-2 gene for arylamine N-acetyltransferase	2e-23	171200	(J04734) CDC6 protein [Saccharomyces cerevisiae]	8.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens MLL-				
1480	AF024541	AF4 fusion protein mRNA, partial cds	2e-23	2136142	serine/proline-rich FEL protein, splice form 1 - human	1e-20
1481	L13773	Human AF-4 mRNA, complete cds.	2e-23	3063962	(AF031404) MLL-AF4 fusion protein [Homo sapiens]	1e-20
1482	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-24	<NONE>	<NONE>	<NONE>
1483	U75467	Drosophila melanogaster Rga and Atu genes, complete cds	8e-24	1658503	(U75467) Atu [Drosophila melanogaster]	2e-37
1484	D17076	Human HepG2 partial cDNA, clone hmd5a09m5	7e-24	<NONE>	<NONE>	<NONE>
1485	AF100694	Mus musculus Pontin52 mRNA, complete cds	7e-24	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis] (Z81054) predicted using Genefinder; Similarity to UDP-glucuronosyltransferases	7e-10
1486	M11167	Human 28S ribosomal RNA gene.	2e-24	3875481	USP1 PROTEIN PRECURSOR >gi 169623	1.2
1487	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-24	549173	(X65335) lacZ gene product [unidentified cloning vector]	0.058
1488	AB003468	Cloning vector pAP3neo DNA, complete sequence	2e-24	987050	(M74509) [Human endogenous retrovirus type C oncovirus sequence.], gene product [Homo sapiens]	3e-04
1489	X03541	Human mRNA of trk oncogene >:: gb 196186 196186 Sequence 23 from patent US 5734039	2e-24	325465	reverse transcriptase related protein [Homo sapiens]	4e-12
1490	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	2e-24	225047	(U95760) Sno [Drosophila melanogaster]	2e-41
1491	U95760	Drosophila melanogaster strawberry notch (sno) mRNA, complete cds	2e-24	2078282	(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	8.6
1492	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-25	2623773		

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1493	AB002405	Homo sapiens mRNA for LAK-4p, complete cds	8e-25	2496822	HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOME X >gi 746502 (U23516) B0416.1 gene product [Caenorhabditis elegans]	9e-11
1494	K03002	Human mRNA from chromosome 15 gene with homology to MHC-HLA-SB-1 intron A.	8e-25	1514614	(X92842) nuclear protein [Mus musculus]	1e-13
1495	U61232	Human tubulin-folding cofactor E mRNA, complete cds	7e-25	1465772	(U61232) cofactor E [Homo sapiens]	2e-05
1496	U10245	Arabidopsis thaliana Col-O putative RNA helicase A mRNA, complete cds.	5e-25	1353239	(U10245) putative RNA helicase A [Arabidopsis thaliana]	1e-37
1497	X89211	H.sapiens DNA for endogenous retroviral like element	3e-25	2065210	(Y12713) Pro-Pol-dUTPase polyprotein	5e-06
1498	L81652	Homo sapiens (subclone 2_g11 from P1 H43) DNA sequence	3e-25	2072961	(U93568) putative p150 [Homo sapiens]	5e-16
1499	X82895	H.sapiens mRNA for DLG2	2e-25	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS, LARGE HOMOLOG 2)	1e-34
1500	M36654	Mouse homeo box 2.6 (Hox-2.6) mRNA, complete cds.	9e-26	3323169	(AE001255) T. pallidum predicted coding region TP0854	1.9
1501	L36315	Mus musculus (clone pMLZ-1) zinc finger protein	9e-26	1806134	(Z67747) zinc finger protein [Mus musculus]	4e-05
1502	AB018281	Homo sapiens mRNA for KIAA0738 protein, complete cds	9e-26	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1503	AF017433	Homo sapiens putative transcription factor CR53	9e-26	3219985	ZINC FINGER PROTEIN ZFP-29	1e-17

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens (subclone 2_e6 from BAC H94) DNA sequence				
1504	AC001225		8e-26	2653713	(U91823) small S protein [Hepatitis B virus]	4.3
1505	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-26	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	3.4
1506	X94912	H.sapiens Pr22 gene	3e-26	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	4e-09
1507	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-26	<NONE>	<NONE>	<NONE>
1508	U44103	Human small GTP binding protein Rab9 mRNA, complete cds	1e-26	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	8.7
1509	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.14
1510	AG001212	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	9e-27	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.012
1511	AF027131	Mus musculus mucin glycoprotein MUC3 mRNA, partial cds	9e-27	2589172	(U76551) mucin Muc3 [Rattus norvegicus]	2e-14
1512	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	5e-27	1438534	(U49057) rA9 [Rattus norvegicus]	1e-04
1513	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to 9.	3e-27	<NONE>	<NONE>	<NONE>
1514	Z78160	M.musculus partial cochlear mRNA (clone 28D2)	3e-27	1490362	(Z78160) unknown [Mus musculus]	2e-05
1515	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.r1a.	3e-27	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	1e-06

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1516	L35659	(subclone H8 6_h6 from P1 35 H5 C8) DNA sequence.	1e-27	<NONE>	<NONE>	<NONE>
1517	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	1644471	(U72686) odorant receptor 4 (Danio rerio)	7.5
1518	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2738388	(AF003534) hypothetical protein 004L [Chilo iridescent virus]	6.7
1519	AB009271	Homo sapiens gene for BCNT, partial cds	1e-27	3880909	(AL032636) Y40B1B.3 [Caenorhabditis elegans]	4.6
1520	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.85
1521	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	121805	ENDOGLUCANASE A PRECURSOR	0.58
1522	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3722000	(AF035323) survival motor neuron protein [Bos taurus]	0.10
1523	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	3328188	(AF074902) laminin alpha chain [Caenorhabditis elegans]	0.083
1524	AF074382	Homo sapiens Ikb kinase gamma subunit	1e-27	3641280	(AF074382) Ikb kinase gamma subunit [Homo sapiens]	0.041
1525	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-27	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1526	L78778	Homo sapiens (subclone 2_e10 from P1 H49) DNA sequence	1e-27	225047	reverse transcriptase related protein [Homo sapiens]	2e-09
1527	L03427	Human zinc finger protein basonuclein mRNA, complete cds.	1e-27	1488275	(U59694) zinc finger protein basonuclein [Homo sapiens]	9e-22
1528	U09954	Human ribosomal protein L9 gene, 5' region and complete cds.	4e-28	2257538	(AB004538) LIPOIC ACID SYNTHETASE PRECURSOR(LIP-SYN) [Schizosaccharomyces pombe]	2e-04

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1529	Z64210	H.sapiens CpG DNA, clone 99b4, reverse read cpg99b4.rt1a.	4e-28	3878570	(Z46381) similar to lipoic acid synthase; cDNA EST yk283b6.3 comes from this gene; cDNA EST yk283b6.5 comes from this gene; cDNA EST yk472f5.3 comes from this gene; cDNA EST yk472f5.5 comes from this gene; cDNA EST yk476e7.3...	7e-11
1530	U55177	Danio rerio carbonic anhydrase homolog CAH-Z mRNA, complete cds	4e-28	3123190	CARBONIC ANHYDRASE (CARBONATE DEHYDRATASE) >gi 2576335 (U55177) CAH-Z (Danio rerio)	5e-21
1531	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-28	1351839	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) >gi 930358 taurus]	3e-27
1532	AF016591	Homo sapiens survival motor neuron pseudogene, complete sequence	3e-28	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-08
1533	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	2.5
1534	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.004
1535	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	6e-04
1536	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-05

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1537	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1538	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-09
1539	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-09
1540	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1541	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-11
1542	AF100694	Mus musculus Pontin52 mRNA, complete cds	2e-28	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	8e-12
1543	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1544	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1545	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1546	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1547	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1548	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1549	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1550	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1551	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1552	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1553	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1554	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1555	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1556	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1557	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1558	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1559	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1560	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1561	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
1562	AF100694	Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1563	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1564	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1565	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1566	M87708	Human simple repeat polymorphism.	1e-28	<NONE>	<NONE>	<NONE>
1567	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	<NONE>	<NONE>	<NONE>
1568	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AF100694) similar to raminin B; cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID e1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	3.0
1569	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.66

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1570	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	3924779	(AL000505) similar to laminin B, cDNA EST yk450d8.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes fr... >gi 3924881 gnl PID c1354569 from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk219a2.5 comes from this gene; cDNA EST yk355e4.5 comes from this gene; cDNA EST yk224f4.5 comes from...	0.65
1571	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1572	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.49
1573	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	283446	cyteine-rich surface antigen 72, CRP72 - Giardia lamblia (fragment)	0.45
1574	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2498937	SPERMATOPHORIN SP23 PRECURSOR mealworm >gi 161725 (M92928) structural protein	0.33
1575	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.18
1576	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	2133579	spermatophorin Sp23 - yellow mealworm molitor]	0.088
1577	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.018
1578	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.016

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1579	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.012
1580	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.010
1581	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1582	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	0.002
1583	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1584	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.002
1585	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1586	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.001

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1587	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.001
1588	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-04
1589	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1590	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-04
1591	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	2e-04
1592	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-04
1593	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1594	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-05
1595	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1596	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05
1597	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-06
1598	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-06
1599	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-06
1600	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens]	4e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1601	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1602	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06
1603	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	9e-07
1604	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	8e-07
1605	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	1169643	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related peptide [Lymnaea stagnalis]	7e-07
1606	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-07
1607	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-07

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1608	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-07
1609	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1610	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-07
1611	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-08
1612	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-08
1613	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-09

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1614	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-09
1615	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-09
1616	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	7e-10
1617	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	6e-10
1618	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-10
1619	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	4e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1620	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-10
1621	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	5e-11
1622	AF100694	Mus musculus Pontin52 mRNA, complete cds	1e-28	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-12
1623	AF032896	Petromyzon marinus polyadenylate binding protein	1e-28	1082703	polyadenylate binding protein II human	2e-27
1624	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.013
1625	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	2133579	spermatophorin Sp23 - yellow mealworm molitor]	6e-04
1626	AF100694	Mus musculus Pontin52 mRNA, complete cds	9e-29	3876465	(Z81071) predicted using Genefinder; Similarity to Human small nuclear ribonucleoprotein E cDNA EST yk375g7.5 comes from this gene; cDNA EST yk435f5.3 comes from this gen...	9e-06
1627	AF100694	Mus musculus Pontin52 mRNA, complete cds	8e-29	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-06

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ADP-RIBOSYLATION	
1628	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	728883	FACTOR 3 fruit fly (Drosophila melanogaster) >gi507234 (L25063) ADP ribosylation factor 3 [Drosophila melanogaster]	0.016
1629	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	544357	RNA-BINDING PROTEIN FUS/TLS protein [human, Peptide, 526 aa] [Homo sapiens] (AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	2e-07
1630	AF100694	Mus musculus Pontin52 mRNA, complete cds	4e-29	4056454	ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCAD) dehydrogenase precursor - rat Acyl-CoA dehydrogenase [Rattus norvegicus]	1e-08
1631	D43682	Human mRNA for very-long-chain acyl-CoA dehydrogenase (VLCAD), complete cds	4e-29	1168287	(Z95556) accD1 [Mycobacterium tuberculosis]	6e-37
1632	Y07660	M.tuberculosis accBC gene	4e-29	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	3e-47
1633	X55367	Human alpha-satellite DNA from clone pTRA-2.	1e-29	<NONE>	<NONE>	<NONE>
1634	L81866	Homo sapiens (subclone 1_f1 from P1 H54) DNA sequence	1e-29	<NONE>	<NONE>	<NONE>
1635	S75940	{Alu repeats, clone 52H10} [human, colonic mucosa, Genomic, 943 nt]	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-07
1636	AB001907	Homo sapiens PACE4 gene, exon 13	1e-29	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-09
1637	AF077003	Mus musculus SH3 domain-containing adapter protein mRNA, complete cds	5e-30	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1638	AF100694	Mus musculus PontinS2 mRNA, complete cds	4e-30	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	3e-10
1639	M27072	Xenopus laevis poly(A)-binding protein (ABP-EF) mRNA, complete cds.	4e-30	1352709	POLYADENYLATE-BINDING PROTEIN polyadenylate-binding protein - African clawed frog laevis]	5e-21
1640	X58386	B.taurus mRNA for bovine vacuolar ATPase subunit A	2e-30	2773154	(AF039573) abscisic acid- and stress-inducible protein	4.3
1641	Y07660	M.tuberculosis accBC gene	1e-30	2113935	(Z95556) accD1 [Mycobacterium tuberculosis]	4e-47
1642	AJ236940	Sus scrofa mRNA for hypothetical protein (5': clone 7C4)	4e-31	4102021	(AF007561) delta 6-desaturase [Borago officinalis]	7.4
1643	AF039400	Homo sapiens calcium-dependent chloride channel-1 (hCLCA1) mRNA, complete cds	2e-31	3721912	(AB017156) gob-5 [Mus musculus]	7e-08
1644	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA sequence.	1e-31	461663	BOMBYXIN B-2 HOMOLOG PRECURSOR silkmoth >gi 217385 gnl PID d1003528 (D13924) Samia bombyxin homolog B-2 [Samia cynthia]	1.1
1645	X61971	H.sapiens mRNA for macropain subunit delta	1e-31	296734	(X61971) macropain subunit delta [Homo sapiens]	3e-06
1646	L00016	human mitochondrial trnas and partial proteins 4 & 5; histidyl-, seryl-, leucyl-trna genes: urf4 and urf5 (partial).	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	0.002
1647	M17887	Human acidic ribosomal phosphoprotein P2 mRNA, complete cds.	5e-32	4056454	(AC005990) Contains repeated region with similarity to gb U43627 extensin (atExt1) gene from Arabidopsis thaliana. ESTs gb Z34165 and gb Z18788 come from this gene. [Arabidopsis thaliana]	1e-05

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1659	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	6e-34	3395443	(AC004683) putative ammonium transporter, 3' partial	4.7
1660	AF013988	Homo sapiens serine protease mRNA, complete cds	4e-34	2507226	PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (R-PTP-EPSILON) >gi 1439605 (U62387) protein tyrosine phosphatase-e [Mus musculus]	3.2
1661	U53446	Human mitogen-responsive phosphoprotein DOC-2 mRNA, complete cds.	2e-34	104757	LEP100 protein precursor - chicken >gi 212254 gallus]	1.6
1662	AJ233632	Homo sapiens endogenous retroviral sequence ERV-L pol gene, clone ERV-L Human6	2e-34	3860513	(AJ233597) reverse transcriptase [Mus famulus]	4e-10
1663	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	8e-35	2947070	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]	2.3
1664	X17206	Human mRNA for LLRep3	3e-35	730652	40S RIBOSOMAL PROTEIN S2 (STRINGS OF PEARLS PROTEIN) >gi 1085158 pir S50325 ribosomal protein S2 - fruit fly (Drosophila melanogaster) >gi 515972 (U01335) ribosomal protein S2	2e-10
1665	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	3e-35	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	2e-16
1666	U62801	Human protease M mRNA, complete cds	2e-35	3929231	(AF091247) potassium channel [Rattus norvegicus]	1.0
1667	AF020760	Homo sapiens serine protease (Omi) mRNA, complete cds	1e-35	2738915	(AF020760) serine protease [Homo sapiens]	9e-14

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1668	Z93943	sequence from cosmid U235H3 on chromosome X	8e-36	1196432	(M22333) unknown protein [Homo sapiens]	3e-10
1669	X06778	Rabbit 18S rRNA	7e-36	118588	DEHYDRIN DHN3 >gi 100035 pir S18139 dehydrin DHN3 - garden pea >gi 20709 (X63063) pea dehydrin DHN3 [Pisum sativum]	0.011
1670	AB007962	Homo sapiens mRNA, chromosome 1 specific transcript KIAA0493	3e-36	3329243	(AE001350) hypothetical protein [Chlamydia trachomatis]	3.1
1671	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	141103	HYPOTHETICAL PROTEIN ORF-1137 mouse	0.038
1672	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	3e-36	198651	(M29325) ORF1 [Mus musculus]	0.006
1673	U49082	Human transporter protein (g17) mRNA, complete cds	3e-36	1840045	(U49082) transporter protein [Homo sapiens]	2e-15
1674	J03133	Human transcription factor SP1 mRNA, 3' end.	3e-36	477133	HF-1 regulatory element binding protein - rat	2e-31
1675	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-36	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	4e-37
1676	M34857	Mouse Hox-2.5 mRNA.	9e-37	106296	homeotic protein Hox B9 - human (fragment)	0.15
1677	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	9e-37	2072960	(U93568) p40 [Homo sapiens]	3e-05
1678	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	8e-37	4185944	(Y17833) env protein [Human endogenous retrovirus K]	1e-15

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
1679	Z93943	sequence from cosmid U235H3 on chromosome X	9e-38	106322	hypothetical protein (LIH 3' region) - human	4e-13
1680	X97303	H.sapiens mRNA for Ptg-12 protein	4e-38	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S-4909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	3e-37
1681	Y08999	H.sapiens mRNA for Sop2p-like protein	3e-38	3334339	SOP2-LIKE PROTEIN	5e-06
1682	Z62887	H.sapiens CpG DNA, clone 74g6, forward read cpg74g6.ft1a.	2e-38	1245686	(U53181) F36D4.2 gene product [Caenorhabditis elegans]	0.19
1683	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase region mRNA, partial cds	1e-38	59977	(Z14310) tripartite fusion transcript PLA2L [Human endogenous retrovirus]	1e-06
1684	D86974	Human mRNA for KIAA0220 gene, partial cds	1e-38	3337386	(AC002544) Unknown gene product splice form-2 [Homo sapiens]	8e-11
1685	M31013	Human nonmuscle myosin heavy chain (NMHC) mRNA, 3' end.	1e-38	4115748	(AB022023) nonmuscle myosin heavy chain B	2e-11
1686	AF006087	Homo sapiens Arp2/3 protein complex subunit p20-Arc (ARC20) mRNA, complete cds	4e-39	<NONE>	<NONE>	<NONE>
1687	X58374	D.melanogaster crn mRNA	4e-39	2653888	(AL009171) 62D9.a [Drosophila melanogaster]	4e-42
1688	D85815	Human DNA for rhoHP1, complete cds	1e-39	134080	GTP-BINDING PROTEIN TC10 ras-like protein [Homo sapiens]	3e-26

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1689	U49057	Rattus norvegicus CTD-binding SR-like protein rA9 mRNA, complete cds	4e-40	1438534	(U49057) rA9 [Rattus norvegicus]	5e-05
1690	Y08999	H.sapiens mRNA for Sop2p-like protein	4e-40	3334339	SOP2-LIKE PROTEIN	9e-08
1691	AB002293	Human mRNA for KIAA0295 gene, partial cds	4e-40	2224531	(AB002293) KIAA0295 [Homo sapiens]	1e-30
1692	AF086222	Homo sapiens full length insert cDNA clone ZC66E08	1e-40	2829669	DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1) >gi 1707502 gnl PID e254627 (X99227) double-stranded RNA-specific editase [Homo sapiens] editase 1 hRED1-L [Homo sapiens] >gi 2039300 (U76421) dsRNA adenosine deaminase DRADA2b [Homo sapiens]	0.61
1693	AF044127	Homo sapiens peroxisomal short-chain alcohol dehydrogenase (SCAD-SRL) mRNA, complete cds	1e-40	4105190	(AF044127) peroxisomal short-chain alcohol dehydrogenase	2e-06
1694	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1695	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	6e-23
1696	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1697	U36778	Mus musculus Sil mRNA, complete cds	1e-40	88608	SIL protein - human >gi 338088 (M74558) SIL	5e-23
1698	AB018285	Homo sapiens mRNA for KIAA0742 protein, partial cds	1e-40	3882205	(AB018285) KIAA0742 protein [Homo sapiens]	6e-31

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					ATP-BINDING CASSETTE	
1699	X75927	M.musculus abc2 mRNA	1e-40	728773	TRANSPORTER 1 ABC1 - human >gi 495257 (X75926) abc1 [Mus musculus]	3e-37
1700	AF038200	Homo sapiens clone 23954 mRNA sequence	5e-41	3211975	(AF068195) putative glioblastoma cell differentiation-related protein [Homo sapiens]	5e-14
1701	U20521	Human estrogen sulfotransferase (STE) gene, exon 8 and complete cds	4e-41	<NONE>	<NONE>	<NONE>
1702	AF026548	Homo sapiens branched chain alpha-ketoacid dehydrogenase kinase precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-41	3182923	[3-METHYL-2-OXOBUTANOATE DEHYDROGENASE (LIPOAMIDE)] KINASE PRECURSOR alpha-ketoacid dehydrogenase kinase precursor [Homo sapiens]	2e-09
1703	Y07660	M.tuberculosis accBC gene	2e-41	465847	HYPOTHETICAL 66.5 KD PROTEIN F02A9.5 IN CHROMOSOME III >gi 280542 pir S28313 hypothetical protein F02A9.5 - Caenorhabditis elegans Genefinder: similar to Propionyl-CoA carboxylase beta chain; cDNA EST EMBL:M89018 comes from this gene; cDNA EST EMBL:D28069 comes from this gene; cDNA EST EMBL:D28068 comes from this gene; cDNA EST ...	3e-38
1704	AG001237	Homo sapiens genomic DNA, 21q region, clone: 9H11N46	1e-41	106322	hypothetical protein (L1H 3' region) - human	5e-09
1705	AB007934	Homo sapiens mRNA for KIAA0465 protein, partial cds	1e-41	3413892	(AB007934) KIAA0465 protein [Homo sapiens]	3e-12
1706	AF055029	Homo sapiens clone 24711 mRNA sequence	5e-42	3250681	(AL024486) putative protein	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1707	Z49747	O.cuniculus mRNA for phospholipase C	5e-42	130227	PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-III) >gi 163538 (M20638) phospholipase C-III [Bos taurus]	5e-36
1708	M93651	Human set gene, complete cds.	2e-42	<NONE>	<NONE>	<NONE>
1709	AJ236940	Sus scrofa mRNA for hypothetical protein (5' clone 7C4)	2e-42	2062403	(U79010) delta 6 desaturase [Borago officinalis]	8.5
1710	J03634	Human erythroid differentiation protein mRNA	2e-42	1708436	INHIBIN BETA A CHAIN PRECURSOR	2e-10
1711	AJ223777	Mus musculus mRNA for striatin	6e-43	2494917	STRIATIN >gi 1495773 gnl PID e254158	2e-32
1712	AF016411	Homo sapiens potassium channel subunit KCNA3.1B	2e-43	2708514	(AF016411) KCNA3.1B [Homo sapiens]	3e-13
1713	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913)	1e-43	111814	hypothetical protein 3 - rat >gi 56589	2e-06
1714	X82895	H.sapiens mRNA for DLG2	6e-44	2497511	MAGUK P55 SUBFAMILY MEMBER 2 (MPP2 PROTEIN) (DISCS. LARGE HOMOLOG 2)	6e-52
1715	U17077	Human BENE mRNA, partial cds.	3e-44	53912	(X57960) ribosomal protein L7 [Mus musculus] >gi 55489	8e-30
1716	AJ222700	Homo sapiens mRNA for TSC-22 protein	2e-44	<NONE>	<NONE>	<NONE>
1717	J03634	Human erythroid differentiation protein mRNA	2e-44	124279	INHIBIN BETA A CHAIN PRECURSOR PROTEIN (EDF) >gi 87936 pir B24248 inhibin beta-A chain precursor - human >gi 181947 (J03634) erythroid differentiation protein precursor [Homo sapiens] sapiens] >gi 226850 prt 1608260B inhibin beta.A [Homo sapiens]	0.73

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1718	AB014518	Homo sapiens mRNA for KIAA0618 protein, complete cds	7e-45	1911548	(S80864) cytochrome c-like polypeptide sapiens]	1.6
1719	X76808	H.sapiens genomic DNA clone d2	7e-45	868201	(U29380) similar to adenylate cyclase [Caenorhabditis elegans]	2e-09
1720	AB021288	Homo sapiens mRNA for beta 2-microglobulin, complete cds	2e-45	2465521	(U95995) RNA-dependent RNA polymerase [Cryptosporidium parvum]	0.15
1721	X63468	H.sapiens mRNA for transcription factor TFIIE alpha	8e-46	<NONE>	<NONE>	<NONE>
1722	AF019226	Homo sapiens D2-2 mRNA, 3'UTR	7e-46	<NONE>	<NONE>	<NONE>
1723	D31764	Human mRNA for KIAA0064 gene, complete cds	2e-46	3123050	HYPOTHETICAL PROTEIN KIAA0064	1e-15
1724	K02774	Human MHC class II HLA-DR-beta-psi (DW4/DR4) pseudogene, exons 3,4, 5,6, clones cosII-3301 and cosII-801.	1e-46	4185946	(Y17834) gag protein [Human endogenous retrovirus K]	2e-14
1725	X92109	H.sapiens hcgIX gene	9e-47	2498185	BRIDE OF SEVENLESS PROTEIN PRECURSOR >gi 1079166 pir A47550 bride of sevenless precursor - fruit fly (Drosophila virilis) >gi 290216 virilis]	1.4
1726	X93334	H.sapiens mitochondrial DNA, complete genome	8e-47	128753	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 86696 pir A00435 NADH dehydrogenase (ubiquinone)	4e-15
1727	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-47	<NONE>	<NONE>	<NONE>
1728	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	3e-47	4185944	(Y17833) env protein [Human endogenous retrovirus K]	7e-18
1729	Z63594	H.sapiens CpG DNA, clone 87f9, forward read cpg87f9.frla.	1e-47	3322743	(AE001222) T. pallidum predicted coding region TP0454	2.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		R.rattus mRNA for				
1730	X62295	vascular type-I angiotensin II receptor	4e-48	1209756	(U43629) integral membrane protein [Beta vulgaris]	1e-07
1731	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-48	<NONE>	<NONE>	<NONE>
1732	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	4e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1733	AB020712	Homo sapiens mRNA for KIAA0905 protein, complete cds	3e-49	4240299	(AB020712) KIAA0905 protein [Homo sapiens]	2e-20
1734	X62295	R.rattus mRNA for vascular type-I angiotensin II receptor	1e-49	1209756	(U43629) integral membrane protein [Beta vulgaris]	7e-12
1735	AJ007509	Homo sapiens mRNA for E1B-55kDa- associated protein	1e-49	3319956	(AJ007509) E1B-55kDa- associated protein	4e-24
1736	X97303	H.sapiens mRNA for Prg-12 protein	1e-49	466044	HYPOTHETICAL ZINC FINGER PROTEIN ZK686.4 IN CHROMOSOME III >gi 630780 pir S44909 ZK686.4 protein - Caenorhabditis elegans >gi 304346 (L17337) coded for by C. elegans cDNAs GenBank:M88869 and T01933; putative [Caenorhabditis elegans]	8e-31
1737	AF038404	Homo sapiens homolog of Nedd5 (hNedd5) mRNA, complete cds	4e-50	<NONE>	<NONE>	<NON
1738	L43618	Homo sapiens polycystic kidney disease (PKD1) gene, exons 35-42	4e-50	903758	(L43619) polycystic kidney disease 1 protein [Homo sapiens]	3e-1
1739	AF009424	Homo sapiens clone 22 mRNA, alternative splice variant alpha-1, complete cds	4e-50	2271473	(AF009426) clone 22 [Homo sapiens]	5e

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1740	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA sequence.	2e-50	99758	monosaccharid transport protein STP4 - Arabidopsis thaliana >gi 16524 (X66857) sugar transport protein [Arabidopsis thaliana]	6.4
1741	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA sequence.	2e-50	2072960	(U93568) p40 [Homo sapiens]	2e-05
1742	U80745	Homo sapiens CTG7a mRNA, partial cds	1e-50	<NONE>	<NONE>	<NONE>
1743	D84514	Bovine mRNA for p97, partial cds	1e-50	3978527	(AF103728) structural polyprotein [Sindbis virus]	9.9
1744	M22960	Human protective protein mRNA, complete cds.	1e-50	131081	LYSOSOMAL PROTECTIVE PROTEIN PRECURSOR (CATHEPSIN A) (CARBOXYPEPTIDASE C) human >gi 190283 (M22960) protective protein precursor	1e-12
1745	X86018	H.sapiens mRNA for MUF1 protein	1e-50	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	1e-21
1746	U03495	Human transcription factor LSF-ID mRNA, complete cds.	7e-51	2136296	transcription factor LSF - human >gi 476099	1e-21
1747	AB015344	Homo sapiens HRIHFB2157 mRNA, partial cds	5e-51	3970874	(AB015344) HRIHFB2157 [Homo sapiens]	2e-35
1748	M93339	Human zinc finger protein mRNA.	4e-51	3024110	MYC-ASSOCIATED ZINC FINGER PROTEIN sapiens]	2e-06
1749	U71363	Human zinc finger protein zfp6 (ZF6) mRNA, partial cds	4e-51	2689441	(AC003682) F1S547_1 [Homo sapiens]	2e-11
1750	X56932	H.sapiens mRNA for 23 kD highly basic protein	4e-51	730451	60S RIBOSOMAL PROTEIN L13A (23 KD HIGHLY BASIC PROTEIN) >gi 345897 pir S29539 basic protein, 23K - human >gi 23691 (X56932) 23 kD highly basic protein [Homo sapiens]	1e-11
1751	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA21E11	2e-51	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens				
1752	AF068245	BAF60b gene, partial sequence	5e-52	<NONE>	<NONE>	<NONE>
1753	AJ236932	Sus scrofa mRNA for hypothetical protein (5': clone 4B8)	5e-52	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1754	AF003693	Mus musculus scaffold protein Pbp1 homolog mRNA, complete cds	6e-53	2197106	(AF003693) scaffold protein Pbp1 homolog [Mus musculus]	2e-54
1755	M27319	Human calmodulin mRNA, complete cds.	5e-53	115528	CALMODULIN >gi 102408 pir JC1309 calmodulin - Stylonychia lemnae (SGC5) >gi 161195	0.002
1756	M74555	Mouse house-keeping protein mRNA, complete cds.	5e-53	284775	house-keeping protein - mouse >gi 193871	5e-30
1757	X92720	H.sapiens mRNA for phosphoenolpyruvate carboxykinase	6e-54	2135915	phosphoenolpyruvate carboxykinase (GTP) (EC 4.1.1.32) precursor, mitochondrial - human carboxykinase (GTP) [Homo sapiens]	6e-21
1758	AF007872	Homo sapiens torsinB (DQ1) mRNA, partial cds	2e-54	2760121	(AB002405) LAK-4p [Homo sapiens]	0.27
1759	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	2e-54	1236083	(U49507) Lisch7 [Mus musculus]	3e-27
1760	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13.	1e-55	2370371	(Y14657) hydrophobin [Pleurotus ostreatus] >gi 2982620 gn PID e1283986 (AJ225061) POH2 hydrophobin [Pleurotus ostreatus]	2.0
1761	U83702	Human cytochrome c oxidase subunit VIa gene, exon 3 and complete cds	8e-56	2982994	(AE000682) hypothetical protein [Aquifex aeolicus]	7.0
1762	Y12781	Homo sapiens mRNA for transducin (beta) like 1 protein	7e-56	3021409	(Y12781) transducin (beta) like 1 protein [Homo sapiens]	7e-39

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1763	AB020673	Homo sapiens mRNA for KIAA0866 protein, complete cds	8e-57	2104553	(AF001548) Myosin heavy chain (MHY11) (5'partial) [Homo sapiens]	4e-04
1764	AJ236932	Sus scrofa mRNA for hypothetical protein (5' clone 4B8)	3e-57	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila melanogaster]	4.7
1765	L06900	Human dystrophin gene, intron 1 containing pseudo exon.	1e-58	4185129	(AC005724) unknown protein [Arabidopsis thaliana] thaliana]	7.0
1766	X93334	H.sapiens mitochondrial DNA, complete genome	9e-59	1492050	(U60315) MC107L [Molluscum contagiosum virus subtype 1]	0.17
1767	AF064856	Rattus sp. 7acomp protein mRNA, complete cds	3e-59	3169626	(AF064856) 7acomp protein [Rattus sp.]	2e-31
1768	AF081484	Homo sapiens alpha-tubulin isoform 1 mRNA, complete cds	2e-59	32015	(X06956) alpha-tubulin [Homo sapiens]	4e-22
1769	X71427	Homo sapiens mRNA for FUS-CHOP protein fusion	1e-60	746557	(U23523) histidine-rich [Caenorhabditis elegans]	0.45
1770	AF013988	Homo sapiens serine protease mRNA, complete cds	1e-60	2564316	(AB006622) No similarities to any reported proteins [Homo sapiens]	0.26
1771	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	7e-61	2137490	lymphocyte specific helicase - mouse musculus]	3e-25
1772	X93334	H.sapiens mitochondrial DNA, complete genome	4e-61	70656	ubiquitin / ribosomal protein S27a - human extension protein, HUBCEP80 [human. Peptide, 156 aa] ubiquitin extention protein [Cavia porcellus]	9e-08
1773	D38255	Homo sapiens mRNA for CAB1, complete cds	4e-61	2135214	gene MLN 64 protein - human	4e-23
1774	U25691	Mus musculus lymphocyte specific helicase mRNA, complete cds	8e-62	2137490	lymphocyte specific helicase - mouse musculus]	8e-26

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1775	M21731	Human lipocortin-V mRNA, complete cds.	6e-62	3212603	Human Annexin V With Proline Substitution By Thioproline	2e-20
1776	AF021936	Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta (MRCK-beta) mRNA, complete cds	2e-62	2736153	(AF021936) myotonic dystrophy kinase-related Cdc42-binding kinase MRCK-beta [Rattus norvegicus]	3e-27
1777	Y12059	H.sapiens HUNKI mRNA	1e-62	3184498	(AC004798) R31546_1 [Homo sapiens]	3e-09
1778	L37368	Human (clone E5.1) RNA-binding protein mRNA, complete cds.	6e-63	477578	sialidase - Actinomyces viscosus >gi 141852	7.8
1779	M27877	Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.	5e-63	1731443	ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1) >gi 106023 pir A32891 finger protein 1, placental - human	3e-33
1780	AF095448	Homo sapiens putative G protein-coupled receptor	2e-63	3116131	(AL023288) hypothetical protein	4.6
1781	L19437	Human transaldolase mRNA containing transposable element, complete cds	2e-63	1533119	(U63159) transaldolase [Mus musculus]	4e-18
1782	L41351	Homo sapiens prostatic mRNA, complete cds	1e-63	2833277	PROSTASIN PRECURSOR precursor - human >gi 862305 (L41351) prostatic (Homo sapiens) >gi 1143194 (U33446) prostatic [Homo sapiens]	6e-14
1783	AF053470	Homo sapiens 10kD protein (BC10) mRNA, complete cds	6e-64	482237	hypothetical protein K03H1.9 - Caenorhabditis elegans	0.029

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1784	D37791	Mouse mRNA for beta-1,4-galactosyltransferase	6e-64	3880102	(Z93390) similar to FYVE zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans] zinc finger; cDNA EST yk265b4.5 comes from this gene; cDNA EST yk359g9.5 comes from this gene; cDNA EST yk319c2.5 comes from this gene [Caenorhabditis elegans]	3e-16
1785	AF015770	Mus musculus radical fringe (radical-fringe) mRNA, complete cds	6e-64	2204355	(U94350) radical fringe precursor [Mus musculus]	1e-36
1786	Z79054	H.sapiens flow-sorted chromosome 6 HindIII fragment. SC6pA21E11	2e-64	<NONE>	<NONE>	<NONE>
1787	M83094	Homo sapiens cytosolic selenium-dependent glutathione peroxidase gene, complete cds, and rho12 gene, 3' end.	1e-64	2447063	(U42580) A565R [Paramecium bursaria Chlorella virus 1]	8.8
1788	Y10211	H.sapiens LAG-3 gene, promoter region	7e-65	1944540	(X14112) tegument protein [human herpesvirus 1]	2.3
1789	M19045	Human lysozyme mRNA, complete cds.	2e-65	<NONE>	<NONE>	<NONE>
1790	U01882	Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds	2e-65	585401	LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN) >gi 480045 pir S36249 lipB protein - Pseudomonas glumae >gi 49207 (X70354) helper protein	4.2
1791	AF069517	Homo sapiens RNA binding protein DEF-3 mRNA, complete cds	2e-65	3212101	(AF069517) RNA binding protein DEF-3 [Homo sapiens]	1e-25

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Homo sapiens jerky gene product homolog mRNA, complete cds				
1792	AF004715		2e-65	2314829	(AF004715) jerky gene product homolog [Homo sapiens]	2e-45
1793	X59652	C. longicaudatus hprt mRNA for hypoxanthine	3e-66	631625	hypoxanthine (guanine) phosphoribosyltransferase - long tailed hamster phosphoribosyltransferase [Cricetulus longicaudatus]	6e-54
1794	U94350	Mus musculus radical fringe precursor mRNA, complete cds	3e-67	2204355	(U94350) radical fringe precursor [Mus musculus]	2e-33
1795	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	3e-68	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	7e-51
1796	J03137	Cow phosphoinositide-specific phospholipase C	3e-69	226908	phospholipase C 154 [Bos taurus]	3e-25
1797	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	1e-69	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	2e-33
1798	AF015811	Mus musculus putative lysophosphatidic acid acyltransferase mRNA, complete cds	4e-70	2317725	(AF015811) putative lysophosphatidic acid acyltransferase [Mus musculus]	3e-19
1799	X65157	M. musculus mRNA for desmoyokin, partial	5e-74	109781	desmoyokin - mouse (fragment) >gi50675	9e-37
1800	Z97207	Mus musculus mRNA for B-IND1 protein	2e-74	2231019	(Z97207) B-IND1 protein [Mus musculus]	6e-21
1801	U27196	Gallus gallus zinc finger protein (Fzf-1) mRNA, complete cds	6e-75	984814	(U27196) zinc finger protein [Gallus gallus] gallus	2e-44

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					70 KD WD-REPEAT TUMOR-SPECIFIC ANTIGEN >gi 2505957 gnl PID e353992 (Y15054) 70 kD tumor-specific antigen [Rattus norvegicus]	
1802	Y15054	Rattus norvegicus mRNA for 70 kDa tumor specific antigen, partial	3e-77	3123027		4e-42
1803	X65157	M.musculus mRNA for desmoyokin, partial	3e-79	109781	desmoyokin - mouse (fragment) >gi 50675	9e-33
1804	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	2e-84	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	7e-30
1805	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	2e-84	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	6e-43
1806	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	6e-85	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-41
1807	U19181	Rattus norvegicus Rabin3 mRNA, complete cds.	2e-87	624225	(U19181) Rabin3 [Rattus norvegicus]	2e-41
1808	U40342	Mus musculus ninein mRNA, complete cds.	1e-91	1113865	(U40342) ninein [Mus musculus]	2e-36
1809	X67877	R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein	4e-92	136077	TROPOMYOSIN BETA 3, FIBROBLAST chicken >gi 515694 (M23082) tropomyosin [Gallus gallus]	0.56
1810	AF044574	Rattus norvegicus putative peroxisomal 2,4-dienoyl-CoA reductase (DCR-AKL) mRNA, complete cds	5e-93	4105269	(AF044574) putative peroxisomal 2,4-dienoyl-CoA reductase [Rattus norvegicus]	1e-50
1811	AF035527	Mus musculus EHF (Ehf) mRNA, complete cds	2e-95	3138930	(AF035527) EHF [Mus musculus]	2e-47

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1812	AB016930	Cricetus griseus mRNA for Phosphatidylglycerophosphate synthase, complete cds	6e-96	4159682	(AB016930) Phosphatidylglycerophosphate synthase [Cricetus griseus]	7e-41
1813	AB005549	Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds	7e-97	3868778	(AB005549) atypical PKC specific binding protein [Rattus norvegicus]	3e-41
1814	X90849	G.gallus PB1 gene h-lamp-2=lysosome-associated membrane protein-2 protein-2b (LAMP2) mRNA, alternatively spliced form h-lamp-2b, complete cds.	2e-97	2134381	polybromo 1 protein - chicken chicken >gi 951231 (X90849) polybromo 1 protein [Gallus gallus]	1e-34
1815	S79873	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	3e-98	<NONE>	<NONE>	<NONE>
1816	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	2e-98	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	9e-39
1817	L14684	Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.	e-100	585084	ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G) >gi 543383 pir S40780 translation elongation factor G, mitochondrial - rat >gi 310102	2e-30
1818	X84692	M.musculus Spnr mRNA for RNA binding protein	e-133	1363238	spermatid perinuclear RNA-binding protein Spnr - mouse >gi 673454 (X84692) spermatid perinuclear RNA binding protein [Mus musculus]	5e-35
1819	U50736	Rattus norvegicus cardiac adriamycin responsive protein mRNA, complete cds	e-113	1362781	cytokine inducible nuclear protein C193 - human >gi 793841 (X83703) nuclear protein [Homo sapiens]	2e-36
1820	S66855	HoxB9=Hox-2.5 [mice, embryos, mRNA Partial, 786 nt]	e-107	1708355	HOMEBOX PROTEIN HOX-B9 (HOX-2.5)	8e-37

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HoxB9=Hox-2.5				
1821	S66855	[mice, embryos, mRNA Partial, 786 nt]	e-108	1708355	HOMEODOMAIN PROTEIN HOX-B9 (HOX-2.5)	4e-37
1822	U92072	Rattus norvegicus m-tomosyn mRNA, complete cds	e-102	3790389	(U92072) m-tomosyn [Rattus norvegicus]	2e-38
1823	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-129	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	2e-39
1824	AF062484	Mus musculus SDP8 mRNA, complete cds	e-122	3126981	(AF062484) SDP8 [Mus musculus]	5e-40
1825	X73683	R.norvegicus mRNA for histone H3.3	e-109	122075	(H3.3Q) histone H3.3 - fruit fly (Drosophila melanogaster) histone H3.3B - chicken >gi 2119023 pir S61218 histone H3.3 - fruit fly (Drosophila hydei) 1-136 [Oryctolagus cuniculus] >gi 8046 (X53822) Histone H3.3Q gene product [Drosophila melanogaster] >gi 51198 gallus] >gi 161190 (M17876) histone H3 [Spizula solidissima] >gi 211853 (M11393) histone 3.3 [Gallus gallus] >gi 306848 (M11354) H3.3 histone [Homo sapiens] melanogaster] >gi 963031 (X81205) histone H3.3 H3.3A variant [Drosophila melanogaster] musculus]	2e-40
1826	U67203	Mus musculus ACF7 neural isoform 1 (mACF7) mRNA, partial cds	e-102	1675224	(U67204) ACF7 neural isoform 2 [Mus musculus]	2e-40
1827	D17577	Mouse mRNA for kinesin-like protein (Kif1b), complete cds	e-131	2497524	KINESIN-LIKE PROTEIN KIF1B mouse >gi 407339 gnl PID d1005029 (D17577) Kif1b [Mus musculus]	7e-42

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1828	AB016930	<i>Cricetus griseus</i> mRNA for Phosphatidylglycerophosphate synthase, complete cds	e-131	4159682	(AB016930) Phosphatidylglycerophosphate synthase [<i>Cricetus griseus</i>]	3e-43
1829	U09874	<i>Mus musculus</i> SKD3 mRNA, complete cds.	e-122	2493735	SKD3 PROTEIN SKD3 [<i>Mus musculus</i>]	7e-48
1830	X99145	<i>C.familiaris</i> mRNA for C3VS protein	e-110	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [<i>Canis familiaris</i>]	2e-49
1831	X99836	<i>P.walti</i> mRNA for rnp associated protein 55	e-106	4200286	(X99836) rap55 [<i>Pleurodeles walti</i>]	2e-50
1832	AF077003	<i>Mus musculus</i> SH3 domain-containing adapter protein mRNA, complete cds	e-121	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	3e-51
1833	AF060246	<i>Mus musculus</i> strain C57BL/6 zinc finger protein 106 (Zfp106) mRNA, H3a-a allele, complete cds	e-118	3372657	(AF060246) zinc finger protein 106 [<i>Mus musculus</i>]	1e-52
1834	Z14030	<i>R.norvegicus</i> mRNA for TRAP-complex gamma subunit.	e-120	1174453	TRANSLUCON-ASSOCIATED PROTEIN, GAMMA SUBUNIT (TRAP-GAMMA) (SIGNAL SEQUENCE RECEPTOR GAMMA SUBUNIT) (SSR-GAMMA) >gi 423185 pir S33294 translocon-associated protein gamma chain - rat norvegicus]	7e-54
1835	AF077003	<i>Mus musculus</i> SH3 domain-containing adapter protein mRNA, complete cds	e-132	3550240	(AF077003) SH3 domain-containing adapter protein; CD2AP	5e-54
1836	L20427	<i>Rattus norvegicus</i> dihydroxypolyprenylbenzoate methyltransferase mRNA, complete cds	e-116	457372	(L20427) dihydroxypolyprenylbenzoate methyltransferase dihydroxypolyprenylbenzoate methyltransferase [<i>Rattus norvegicus</i>]	4e-56

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
1837	X80169	M.musculus mRNA for 200 kD protein	e-122	1717793	PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR) >gi 1083553 pir A55117 tsg24	2e-56
1838	AF080568	Rattus norvegicus CTP:phosphoethanolamine cytidyltransferase mRNA, complete cds	e-119	3396102	(AF080568) CTP:phosphoethanolamine cytidyltransferase	6e-58
1839	X99145	C.familiaris mRNA for C3VS protein	e-121	1429314	(X99145) overexpressed in thyroid tissue after TSH stimulation [Canis familiaris]	2e-58
1840	AF019075	Pan troglodytes breast and ovarian cancer susceptibility (BRCA1) gene, partial cds	e-145	2218154	(AF005068) breast and ovarian cancer susceptibility protein splice variant [Homo sapiens]	1e-58
1841	U55042	Bos taurus myosin X, complete cds	e-122	1755049	(U55042) myosin X [Bos taurus]	1e-61
1842	AJ007780	Mus musculus mRNA for poly(ADP-ribose) polymerase-2	e-119	3283975	(AF072521) poly-(ADPribosyl)-transferase homolog PARP	4e-62
1843	AF072865	Rattus norvegicus thioredoxin reductase (TrxR2) mRNA, nuclear gene encoding mitochondrial protein, complete cds	e-105	3757888	(AF072865) thioredoxin reductase [Rattus norvegicus]	3e-62
1844	U55042	Bos taurus myosin X, complete cds	e-121	1755049	(U55042) myosin X [Bos taurus]	1e-62
1845	X61506	Mouse E46 mRNA for E46 protein	e-139	114909	BRAIN PROTEIN E46	9e-67
1846	D90335	Bovine mRNA for GTP-binding protein alpha-subunit	e-143	585174	GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-14 SUBUNIT (GL1) >gi 108711 pir A40891 GTP-binding protein GL1 alpha chain - bovine protein, alpha-subunit [Bos taurus]	2e-69
1847	U49507	Mus musculus B6CBA Lisch7 mRNA, partial cds.	e-140	2121326	(AC002128) Lisch7 [Homo sapiens]	2e-74

Table 4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
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2	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
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21	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
22	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>	<NONE>
23	<NONE>	<NONE>	<NONE>	1079469	rMDC I protein - crab-eating macaque	9.3
24	<NONE>	<NONE>	<NONE>	3043656	(AB011138) KIAA0566 protein [Homo sapiens]	9.3
25	<NONE>	<NONE>	<NONE>	112175	potassium channel protein RK5 - rat protein [Rattus norvegicus]	8.6
26	<NONE>	<NONE>	<NONE>	3769624	(AF091565) olfactory receptor [Rattus norvegicus]	7.2
27	<NONE>	<NONE>	<NONE>	3876443	(Z81517) F28B1.6 [Caenorhabditis elegans]	7.1
28	<NONE>	<NONE>	<NONE>	2224464	(AB001684) ORF249 [Chlorella vulgaris]	6.9
29	<NONE>	<NONE>	<NONE>	1519707	(U67940) ORFveg106; random cDNA sequence [Dictyostelium discoideum]	6.7
30	<NONE>	<NONE>	<NONE>	227491	protein kinase C II [Xenopus laevis]	6.7
31	<NONE>	<NONE>	<NONE>	630575	C50C3.4 protein - Caenorhabditis elegans	6.0
32	<NONE>	<NONE>	<NONE>	137290	35 KD PROTEIN IN RNA2 clover necrotic mosaic virus >gi 61466 (X08021) ORF for 35 kDa polypeptide (AA 1-317) [Red clover necrotic mosaic virus]	6.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
33	<NONE>	<NONE>	<NONE>	30041	(X16711) pid:g30041 [Homo sapiens]	5.9
34	<NONE>	<NONE>	<NONE>	2493585	CELL DIVISION PROTEIN FTSW	5.7
35	<NONE>	<NONE>	<NONE>	1001450	(D63999) hypothetical protein	5.7
36	<NONE>	<NONE>	<NONE>	3182918	NITROGEN REGULATORY PROTEIN AREA	5.2
37	<NONE>	<NONE>	<NONE>	140011	MITOCHONDRIAL RIBOSOMAL PROTEIN S5 Emericella nidulans mitochondrion (SGC3) >gil12709 nidulans] >gil472822 (J01390) unknown protein	4.3
38	<NONE>	<NONE>	<NONE>	3979943	(AL034393) predicted using Genefinder; similar to WD domain, G-beta repeat; cDNA EST yk362f7.5 comes from this gene; cDNA EST yk362f7.3 comes from this gene [Caenorhabditis elegans]	4.0
39	<NONE>	<NONE>	<NONE>	950203	(U31329) polyketide synthase [Aspergillus terreus]	3.3
40	<NONE>	<NONE>	<NONE>	3560232	(AL031530) hypothetical zinc finger protein [Schizosaccharomyces pombe]	3.0
41	<NONE>	<NONE>	<NONE>	730071	AXONEME-ASSOCIATED PROTEIN MST101(1) product [Drosophila hydei]	2.6
42	<NONE>	<NONE>	<NONE>	2506641	HYPOTHETICAL 21.7 KD PROTEIN IN INTE-PIN INTERGENIC REGION >gil1787402 (AE000214) orf, hypothetical protein [Escherichia coli]	2.5
43	<NONE>	<NONE>	<NONE>	3511232	(AF071556) anthranilate dioxygenase large subunit	2.4
44	<NONE>	<NONE>	<NONE>	1150900	(U43139) envelope glycoprotein gp120 [Human immunodeficiency virus type 1]	1.9
45	<NONE>	<NONE>	<NONE>	3876099	(Z75536) similar to dynein heavy chain; cDNA EST EMBL:D27549 comes from this gene; cDNA EST EMBL:D34859 comes from this gene [Caenorhabditis elegans]	1.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
46	<NONE>	<NONE>	<NONE>	3881150	(AL032647) predicted using Genefinder	1.4
47	<NONE>	<NONE>	<NONE>	132200	COLANIC ACID CAPSULAR BIOSYNTHESIS ACTIVATION PROTEIN A >gi 95605 pir S17701 rcsA protein	1.1
48	<NONE>	<NONE>	<NONE>	2204286	(U61380) germination protein [Bacillus megaterium]	1.0
49	<NONE>	<NONE>	<NONE>	1723955	HYPOTHETICAL 11.4 KD PROTEIN IN FOX1-KEX1 INTERGENIC REGION >gi 2132566 pir S64222 probable membrane protein YGL204c - yeast (Saccharomyces cerevisiae) >gi 1322838 gnl PID e243803 (Z72726) ORF YGL204c [Saccharomyces cerevisiae]	0.84
50	<NONE>	<NONE>	<NONE>	3201564	(AJ006514) prolipoprotein diacylglycerol transferase [Vibrio cholerae]	0.31
51	<NONE>	<NONE>	<NONE>	2808721	(AL021428) hypothetical protein Rv0064	0.27
52	<NONE>	<NONE>	<NONE>	602434	(U17986) GABA/noradrenaline transporter [Homo sapiens]	0.13
53	<NONE>	<NONE>	<NONE>	3347955	(AF076184) cytosolic sorting protein PACS-1b [Rattus norvegicus]	0.12
54	<NONE>	<NONE>	<NONE>	1255887	(U55344) coded for by C. elegans cDNA yk92b4.5; coded for by C. elegans cDNA yk73a1.5; coded for by C. elegans cDNA yk102e9.5; coded for by C. elegans cDNA yk71c8.5; coded for by C. elegans cDNA yk66d11.5; coded for by C. elegans cDNA yk66c3...	0.074
55	<NONE>	<NONE>	<NONE>	103076	Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (Drosophila melanogaster)	0.003
56	<NONE>	<NONE>	<NONE>	107560	Ras inhibitor (clone JC265) - human sapiens]	0.002

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					Bkm-like sex-determining region hypothetical protein CS314 - fruit fly (<i>Drosophila melanogaster</i>)	
57	<NONE>	<NONE>	<NONE>	103076	(AF038604) contains similarity to <i>Drosophila</i> ovarian tumor locus protein (GB:X13693) [<i>Caenorhabditis elegans</i>]	2e-04
58	<NONE>	<NONE>	<NONE>	2702370	(AL033501) phox domain protein [<i>Candida albicans</i>]	6e-05
59	<NONE>	<NONE>	<NONE>	3859713	(AF003386) F59E12.5 gene product [<i>Caenorhabditis elegans</i>]	3e-05
60	<NONE>	<NONE>	<NONE>	2088839	GC-RICH SEQUENCE DNA-BINDING FACTOR GCF - human >gi179412 (M29204) DNA-binding factor [<i>Homo sapiens</i>]	2e-08
61	<NONE>	<NONE>	<NONE>	121059	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...	4e-09
62	<NONE>	<NONE>	<NONE>	3875246	(U64857) No definition line found [<i>Caenorhabditis elegans</i>]	9e-24
63	<NONE>	<NONE>	<NONE>	1465834	(AB014561) KIAA0661 protein [<i>Homo sapiens</i>]	9e-28
64	<NONE>	<NONE>	<NONE>	3327136	(Z66521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:C09217 comes from this gene [<i>Caenorhabditis elegans</i>]	1e-29
65	<NONE>	<NONE>	<NONE>	3880433		8e-31
66	D42133	Rat annexin V gene, exon7 and exon8	5.0	<NONE>	<NONE>	<NONE>
67	L35679	<i>Homo sapiens</i> (subclone H8 2_d11 from P1 35 H5 C8) DNA sequence.	5.0	1086902	(U41278) coded for by <i>C. elegans</i> cDNA yk79g8.5; coded for by <i>C. elegans</i> cDNA cm10c8; coded for by <i>C. elegans</i> cDNA yk79g8.3; similar to leucine-rich repeats found in many proteins [<i>Caenorhabditis elegans</i>]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 strain BX220				
68	U90184	from USA, envelope glycoprotein C2V3 region (env) gene, partial cds	5.0	1297070	(Z71986) convicilin precursor [Vicia narbonensis]	6.6
69	U61465	Human myosin VIIa (MYO7A) gene, 5' exon 37	5.0	2313225	(AE000535) L-lactate permease (lctP) [Helicobacter pylori 26695]	5.0
70	AF013717	Homo sapiens periplakin (PPL) mRNA, partial cds	5.0	3719238	(AF064869) brain-enriched guanylate kinase-associated protein 2; BEGA2 [Rattus norvegicus]	3.8
71	X58245	Soybean mRNA for HMG-1 like protein	5.0	2995363	(AL022245) biotin synthase	0.99
72	AF102425	Fraseria paniculata tRNA-Leu (tmL) gene, intron, chloroplast sequence	4.9	3522958	(AC004411) putative pectinesterase [Arabidopsis thaliana]	6.4
73	X82817	H.sapiens PTP1C/HCP-variant gene	4.9	3875514	(Z81494) cDNA EST EMBL:D27474 comes from this gene; cDNA EST EMBL:D27473 comes from this gene; cDNA EST EMBL:T00471 comes from this gene; cDNA EST EMBL:D34192 comes from this gene; cDNA EST EMBL:D37241 comes from this gene; ...	2.8
74	U04827	Mus musculus brain fatty acid-binding protein	4.9	3676132	(AL031765) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=31.96; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SPTREMBL:Q93319; 2-match_description=HYPOTHETICAL PROTEIN C33A11.2;....	2e-09
75	AF038859	Neospora hughesi strain NE1 internal transcribed spacer 1, complete sequence	4.8	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		M.musculus MFH-1				
76	Y08222	gene	4.8	<NONE>	<NONE>	<NONE>
77	AJ224475	Borrelia burgdorferi left chromosomal subtelomeric region (pfpB gene)	4.8	4218141	(AJ236702) HMR1 protein [Antirrhinum majus]	8.3
78	U02486	Mus musculus LAF putative membrane protein (KRAG) gene, exon 3 and complete cds	4.8	3258103	(AP000006) 367aa long hypothetical protein [Pyrococcus horikoshii]	2.7
79	AB000280	Rat mRNA for peptide/histidine transporter, complete cds	4.8	806317	(M29067) unknown protein [Saccharomyces cerevisiae]	0.001
80	Z49771	A.cepa mitochondrial gene for NADH dehydrogenase subunit 3 and ribosomal protein S12	4.5	<NONE>	<NONE>	<NONE>
81	M63494	Mouse IgG receptor (beta-Fc-gamma-RII) gene, exons 6 and 7, clones lambda-Fc(3.2.93).	4.3	<NONE>	<NONE>	<NONE>
82	Z14035	S.pombe car1 gene	2.0	3790665	(AF099000) No definition line found [Caenorhabditis elegans]	1.2
83	U17129	Rhodococcus erythropolis ThcA (thcA) gene, complete cds; and unknown genes	2.0	2828280	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	2e-26
84	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	2.0	4176500	(AL031177) dJ889M15.3 (novel protein)	9e-59
85	U79292	Human clone 23734 mRNA sequence	1.9	<NONE>	<NONE>	<NONE>
86	V00159	Chloroplast Euglena gracilis gene coding for the 5S and 16S rRNA.	1.9	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
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		Xenopus laevis XL-INCENP (XL-INCENP) mRNA, complete cds	1.9	<NONE>	<NONE>	<NONE>
87	U95094					
88	X93206	H. salinarum TATA box-binding protein genes and ORFs	1.9	<NONE>	<NONE>	<NONE>
		Caenorhabditis elegans programmed cell death specifier (ces-2) gene, complete cds	1.9	<NONE>	<NONE>	<NONE>
89	U60979					
90	X56272	C. tentans ORFs (A-E) for hemoglobin	1.9	<NONE>	<NONE>	<NONE>
		Homo sapiens DNA sequence, repeat region.	1.9	<NONE>	<NONE>	<NONE>
91	L22383					
		Hirudo medicinalis neuron-specific protein mRNA, complete cds	1.9	3822533	(AF094531) immunoglobulin heavy chain precursor	2.0
92	U82814					
		Haplomitrium hookeri 18S rRNA gene, partial sequence.	1.9	1083969	hypothetical protein 6 - fowlpox virus virus]	2.0
93	U18504					
		Pseudomonas stutzeri nosDFY genes involved in copper processing	1.9	2980781	(AL022198) putative protein	0.70
94	X53676					
		Dictyostelium discoideum multidrug resistance transporter/Ser protease (tagC) mRNA, complete cds.	1.9	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	6e-05
95	U60086					
		Human putative G-protein-coupled receptor (GPR17) gene, complete cds	1.9	3880034	(Z75550) similar to cell division control protein [Caenorhabditis elegans]	7e-14
96	U33447					
		Sus scrofa lactoferrin mRNA, complete cds. > :: gb I28421 I28421 Sequence 5 from patent US 5571691	1.8	<NONE>	<NONE>	<NONE>
97	M81327					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>S. iniae</i> lctP & lctO genes and ORF1	1.8	<NONE>	<NONE>	<NONE>
98	Y07622					
99	M60474	Mouse myristoylated alanine-rich C-kinase substrate (MARCKS) mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
100	Y13901	Homo sapiens FGFR-4 gene	1.8	<NONE>	<NONE>	<NONE>
101	U44400	Human Down Syndrome region of chromosome 21, clone A31D6-1D6.	1.8	<NONE>	<NONE>	<NONE>
102	U92808	Ruminococcus albus beta-glucosidase (gluA) mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
103	L25051	Candida albicans argininosuccinate lyase (ARG4) gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
104	AE000546	Helicobacter pylori 26695 section 24 of 134 of the complete genome	1.8	<NONE>	<NONE>	<NONE>
105	J00978	Xenopus laevis major beta-globin gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
106	U41716	Human immunodeficiency virus type 1 isolate JW95-5, vpr gene, complete cds.	1.8	<NONE>	<NONE>	<NONE>
107	X66286	G.gallus mRNA for tensin	1.8	<NONE>	<NONE>	<NONE>
108	U76636	Xenopus calbindin D28k mRNA, complete cds	1.8	<NONE>	<NONE>	<NONE>
109	J00664	rabbit embryonic beta-4-globin gene.	1.8	<NONE>	<NONE>	<NONE>
110	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	1.8	2983160	(AE000693) hypothetical protein [Aquifex aeolicus]	7.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rat troponin T			(Z46595) incomplete interleukin-11 receptor isoform [Homo sapiens]	
111	M80829	cardiac isoform gene, complete cds	1.8	999450		7.3
					BRANCHED-CHAIN AMINO ACID TRANSPORT SYSTEM CARRIER PROTEIN (BRANCHED-CHAIN AMINO ACID UPTAKE CARRIER) >gi 1075007 pir D64056 membrane-associated component, branched amino acid transport system (brnQ) homolog - Haemophilus influenzae (strain Rd KW20) system II carrier protein (brnQ) [Haemophilus influenzae Rd]	
112	D37887	Cyprinus carpio c-myc gene for c-Myc, complete cds	1.8	3023408		7.2
		Homo sapiens G protein-coupled receptor kinase 1 and G protein-coupled receptor kinase 1b (GRK1) gene, alternatively spliced, alternative exon 6, exon 7, and partial cds				
113	AF019765		1.8	498643	(U10270) G-box binding factor 1 [Zea mays]	7.2
		Helicobacter pylori J166 virulence regulon transcriptional activator homolog gene, partial cds, strain-specific genomic sequence B2				
114	AF025967		1.8	3850108	(AL033388) putative calcium-transporting atpase [Schizosaccharomyces pombe]	5.7
					PROBABLE HYDROXYACYLGLUTATHIONE HYDROLASE (GLYOXALASE II) (GLX II) protein [Escherichia coli] >gi 1786406 (AE000130) probable hydroxyacylglutathione hydrolase [Escherichia coli]	
115	U13183	Xenopus laevis (Xwnt-4) mRNA, complete cds.	1.8	2494853		5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
116	S68944	Na+/Cl(-)-dependent neurotransmitter transporter	1.8	2276316	(Z96810) GLYT-1 LIKE [Homo sapiens]	5.5
117	M92905	Rat calcium channel alpha-1 subunit (rbB-I) mRNA, complete cds.	1.8	3165522	(AF067607) Similar to cuticular collagen; C18H7.3	5.5
118	X12429	Xenopus laevis U1 70K gene exon 10	1.8	2735957	(AF015685) reverse transcriptase domain protein (Z81072) similarity to human cyclin A/CDK2-associated protein P19 (RNA polymerase elongation factor) (SW:SKP1_HUMAN); cDNA EST EMBL:T00114 comes from this gene; cDNA EST yk390f1.5 comes from this gene; cDNA EST yk402e11.5 co...	3.3
119	D83333	Mouse hepatitis virus genomic RNA for spike protein, partial cds	1.8	3876559	>gi 3877216 gnl PID e1346850 protein P19 (RNA polymerase elongation factor) gene; cDNA EST yk390f1.5 comes from this gene; cDNA EST yk402e11.5 co...	3.3
120	AF016972	Cervus elaphus REDDEER mitochondrial D-loop, complete sequence	1.8	3878057	(Z99942) similar to von Willebrand factor type A domain; cDNA EST yk412d4.5 comes from this gene; cDNA EST yk412d4.3 comes from this gene	3.2
121	AB010741	Oncorhynchus mykiss mRNA for rtSox24, complete cds	1.8	1730805	HYPOTHETICAL 21.0 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION >gi 2132762 pir S63129 probable membrane protein YNL174w - yeast (Saccharomyces cerevisiae) >gi 1302152 gnl PID e239548 (Z71451) ORF YNL174w [Saccharomyces cerevisiae]	2.5
122	U32844	Haemophilus influenzae Rd section 159 of 163 of the complete genome	1.8	728910	A-TYPE INCLUSION PROTEIN (ATI) camelpox virus >gi 62381 (X69774) 84kDa A-type inclusion protein [unidentified]	1.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
123	U18321	Human ionizing radiation resistance conferring protein mRNA, complete cds.	1.8	2133273	ribosomal protein YS7 homolog <i>Emmericella nidulans</i>	1.4
124	M28668	Human cystic fibrosis mRNA, encoding a presumed transmembrane conductance regulator (CFTR). > :: gb I11500 I11500 Sequence 1 from Patent US 5407796	1.8	90492	filaggrin precursor - mouse (fragment)	0.87
125	AF064553	Mus musculus NSD1 protein mRNA, complete cds	1.8	2501207	PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR >gi 1065461 (U40411) Similar to protein disulfide-isomerase. [<i>Caenorhabditis elegans</i>]	0.87
126	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.8	115131	REGULATORY PROTEIN BRLA (BRISTLE A PROTEIN) >gi 83718 pir A28913 regulatory protein brlA - <i>Emmericella nidulans</i> >gi 168029 (M20631) brlA protein	0.84
127	L42096	Homo sapiens (subclone 10_d2 from P1 H21) DNA sequence.	1.8	2135624	metalloproteinase 1 (EC 3.4.24.-) - human	0.65
128	M37278	R.norvegicus renin gene, exons 1-9.	1.8	4050087	(AF109907) S164 [<i>Homo sapiens</i>]	0.58
129	X82879	Artificial sequences DNA for ART 2 consensus	1.8	310929	(L13442) cysteine-rich extensin-like protein-4 [<i>Nicotiana tabacum</i>]	0.52
130	D89729	Homo sapiens mRNA for CRM1 protein, complete cds	1.8	3559944	(AJ010792) Muc5AC protein [<i>Mus musculus</i>]	0.38
131	U78076	Mus musculus sepiapterin reductase gene, exons 1 and 2	1.8	2984225	(AE000766) enolase-phosphatase E-1 [<i>Aquifex aeolicus</i>]	0.095

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
132	X52133	Paramecium 168G gene for 168G surface protein	1.8	115316	COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) >gi 105686 pir S15435 collagen alpha 1(VIII) chain precursor - (U61944) coded for by C. elegans cDNA yk112f3.5; coded for by C. elegans cDNA cm21d2; coded for by C. elegans cDNA CEESR07F; coded for by C. elegans cDNA yk112f3.3; coded for by C. elegans cDNA CEESR29F [Caenorhabditis elegans]	0.073
133	M77830	Human desmoplakin I mRNA, complete cds.	1.8	1397246	(U43192) myosin II heavy chain [Naegleria fowleri]	1e-04
134	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.8	1353761	(U58748) similar to potential transmembrane domains in S. cerevisiae nuclear division RFT1 protein (SP:P38206)	2e-05
135	AJ005518	Mus musculus somatostatin receptor 2 gene, exon1 and 5' flanking region	1.8	1326350	(AL031174) hypothetical protein	2e-08
136	AF002217	Ralstonia eutropha megaplasmid pHG1 nitric oxide reductase (norB) gene, complete cds	1.8	3393018	(AL033388) 3-oxoacyl-[acyl-carrier-protein]-synthase	2e-08
137	AF039035	Caenorhabditis elegans cosmid C53A3	1.8	3850109	(AL022600) putative mannose-1 phosphate gaunyl transferase [Schizosaccharomyces pombe]	3e-11
138	M81769	S.domesticus immunoglobulin rearranged gamma chain mRNA, VJC region, complete cds.	1.8	3080527	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi 984224 (Z54096) unknown	3e-14
139	Y11106	P.pastoris PYC1 gene	1.8	1175412	(AL021687) putative protein [Arabidopsis thaliana] >gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]	1e-15
140	U87803	Human putative Ca2+/calmodulin-dependent protein kinase kinase gene, 3' flanking region, partial sequence	1.8	2828280		3e-17

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
141	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	1.8	1931647	(U95973) endomembrane protein EMP70 precursor isolog HYPOTHETICAL 75.5 KD PROTEIN C14A4.3 IN CHROMOSOME II >gi 3874230 gnl PID e1351618 protein (Swiss Prot accession number P38376); cDNA EST yk220e10.5 comes from this gene [Caenorhabditis elegans]	2e-20
142	L19708	Rat N-methyl-D-aspartate receptor (NMDAR1) gene, first exon.	1.8	1731181	(281103) predicted using Genefinder; cDNA EST yk303g11.5 comes from this gene; cDNA EST yk303g11.3 comes from this gene [Caenorhabditis elegans]	3e-21
143	Y10728	P.schwarzi mitochondrial cytb gene, partial	1.8	3878644	(AL031177) dJ889M15.3 (novel protein)	1e-28
144	AB006631	Homo sapiens mRNA for KIAA0293 gene, partial cds	1.8	4176500	(AL031177) dJ889M15.3 (novel protein)	7e-45
145	AF106967	Mus musculus I3 protein mRNA, complete cds	1.7	<NONE>	<NONE>	<NONE>
146	AE001073	Archaeoglobus fulgidus section 34 of 172 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
147	U12977	Pseudomonas lemoignei poly(3-hydroxybutyrate) depolymerase A precursor (phaZ5) gene, complete cds, and glycerol-3-phosphate-dehydrogenase homolog, complete cds.	1.7	<NONE>	<NONE>	<NONE>
148	M27038	Mus musculus (SK/CamRk) germline IgK chain gene, J1-5 region.	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens HBF-1				
149	X74142	mRNA for transcription factor	1.7	<NONE>	<NONE>	<NONE>
150	U40830	Streptococcus thermophilus DeoD gene, partial cds and EpsA, EpsB, EpsC, EpsD, EpsE, EpsF, EpsG, EpsH, EpsI, EpsJ, EpsK, EpsL, EpsM, Orf14.9 protein genes, complete cds	1.7	<NONE>	<NONE>	<NONE>
151	L29172	Rabbit Ig germline gamma H-chain (allotype d12,e15) C-region gene. 3' end.	1.7	<NONE>	<NONE>	<NONE>
152	M19045	Human lysozyme mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
153	AE001159	Borrelia burgdorferi (section 45 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
154	L17027	Plasmid pFdA (from Fremyella diplosiphon) DNA sequence, including unidentified cds and stem loop.	1.7	<NONE>	<NONE>	<NONE>
155	U12232	Arabidopsis thaliana Columbia GTP binding protein beta subunit (AGB1) mRNA, complete cds.	1.7	<NONE>	<NONE>	<NONE>
156	D42056	Arabidopsis thaliana ATPK6 mRNA for ribosomal-protein S6 kinase homolog, complete cds	1.7	<NONE>	<NONE>	<NONE>
157	X98117	Rhizobium leguminosarum prsD, prsE, ORF3 genes	1.7	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
158	AF039084	Spinacia oleracea heat shock 70 protein protein, complete cds	1.7	<NONE>	<NONE>	<NONE>
159	Z12651	R.norvegicus gene for catechol methyltransferase	1.7	<NONE>	<NONE>	<NONE>
160	AF002968	Fringilla coelebs mitochondrial control region, partial sequence	1.7	<NONE>	<NONE>	<NONE>
161	AE001160	Borrelia burgdorferi (section 46 of 70) of the complete genome	1.7	<NONE>	<NONE>	<NONE>
162	U67553	Methanococcus jannaschii section 95 of 150 of the complete genome	1.7	<NONE>	<NONE>	<NONE>
163	M86247	S.ruminantium plasmid pS23 DNA.	1.7	<NONE>	<NONE>	<NONE>
164	S74436	oIL-8=interleukin-8 [sheep, spleen cells, mRNA, 1435 nt]	1.7	<NONE>	<NONE>	<NONE>
165	D12719	Candida maltosa ALK7 (CYP52A10) and ALK8 complete cds	1.7	<NONE>	<NONE>	<NONE>
166	U02625	Geotrichum candidum NRRL Y-553 lipase gene, partial cds.	1.7	321245	230k bullous pemphigoid antigen BPM1 - mouse	9.3
167	Z58881	H.sapiens CpG DNA, clone 114a4, reverse read cpg114a4.rt1a.	1.7	1854675	(U66298) bone morphogenetic protein-6 [Rattus norvegicus] LARGE PROLINE-RICH PROTEIN BAT2 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >gi179339 (M33509) HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi179345 (M33518) HLA-B-associated transcript 2 (BAT2) [Homo sapiens]	9.1
168	U43674	Agrobacterium tumefaciens conjugal transfer region 1 genes	1.7	1352066		9.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
169	AL023827	Caenorhabditis elegans cosmid Y12A6A, complete sequence [Caenorhabditis elegans]	1.7	731440	PROTOPORPHYRINOGEN OXIDASE (PPO) yeast (Saccharomyces cerevisiae) >gi 603606 (U18778) Hem14p: protoporphyrinogen oxidase [Saccharomyces cerevisiae] >gi 1403536 gnl PID c249333 (Z71381) protoporphyrinogen oxidase [Saccharomyces cerevisiae]	8.9
170	X69662	X.laevis mRNA for glutathione synthetase, large subunit	1.7	4038057	(AC005897) hypothetical protein [Arabidopsis thaliana]	8.8
171	Z35824	S.cerevisiae chromosome II reading frame ORF YBL063w	1.7	3021450	(Y15515) prd1-a [Hydra vulgaris]	7.0
172	M65139	Cowpea chlorotic mottle virus (CCMV) 1a protein gene, complete cds.	1.7	2506307	COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR 1(XII) chain - chicken >gi 222811 gnl PID d1001160 gallus] >gi 2326442 gnl PID e39435 (X61024) collagen type XII alpha 1 chain [Gallus gallus]	7.0
173	X15065	Drosophila distal BX-C region (bithorax complex) pH189 5' region;	1.7	1723625	HYPOTHETICAL 10.0 KD PROTEIN IN ALPA-GABD INTERGENIC REGION (F87) >gi 1033124 (U36840) ORF_f87 [Escherichia coli] >gi 1788982 (AE000348) orf, hypothetical protein	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
174	Z46255	S.cerevisiae chromosome VI lambda clone.	1.7	3875228	(Z46792) similar to lethal(1) discs large-1 tumor suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB... >gi 3879984 gnl PID e1351767 suppressor protein-like repeats; cDNA EST EMBL:D33495 comes from this gene; cDNA EST EMBL:D35117 comes from this gene; cDNA EST EMBL:D36356 comes from this gene; cDNA EST EMB...	6.7
175	U01066	Human CD4 promoter, partial sequence.	1.7	125448	THYMIDINE KINASE saimiriine herpesvirus 1 (strain 11[Onc]) >gi 60341	6.7
176	U34743	Phalaenopsis sp. 'hybrid SM9108' homeobox protein mRNA, complete cds	1.7	1022918	(U38184) ATPase subunit 6 [Trypanosoma cruzi]	6.7
177	U14662	Baboon herpesvirus HVP2 gB glycoprotein (UL27) gene, complete cds.	1.7	3218378	(AL023862) hypothetical protein SC3F9.07 [Streptomyces coelicolor]	6.7
178	AB017006	Homo sapiens PMS2L15 mRNA, partial cds	1.7	1465855	(U64859) glutamine-rich protein [Caenorhabditis elegans]	6.7
179	U92651	Brassica oleracea var. botrytis tonoplast intrinsic protein bobTIP26-1 mRNA, complete cds	1.7	3023675	DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) dynein heavy chain [Schizosaccharomyces pombe]	6.6
180	AF000634	Lytechinus variegatus notch homolog mRNA, complete cds	1.7	148574	(M58520) endo-1,4-beta-glucanase [Fibrobacter succinogenes]	6.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
181	M92354	Arabidopsis thaliana anthranilate synthase alpha subunit gene, complete cds.	1.7	738308	blue light photoreceptor [Arabidopsis thaliana]	6.5
182	AJ234856	Hordeum vulgare genomic DNA fragment; clone MWG2234.rev	1.7	3142302	(AC002411) Strong similarity to myosin heavy chain gb[Z34293 from A. thaliana. [Arabidopsis thaliana]	6.5
183	U76827	Stercorarius parasiticus bird J33 cytochrome b protein, partial cds	1.7	3413810	(Y17034) Bassoon [Mus musculus]	5.4
184	U05211	Saccharomyces cerevisiae Ttp1p (TTP1) gene, complete cds.	1.7	403173	(L24492) lipoprotein [Rhodococcus erythropolis]	4.9
185	AF076974	Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds	1.7	1170140	PUTATIVE ENDOGLUCANASE TYPE K PRECURSOR (ENDO-1,4-BETA-GLUCANASE) (CELLULASE)	4.1
186	AE000753	Aquifex aeolicus section 85 of 109 of the complete genome	1.7	1169357	DNA ADENINE METHYLASE site-specific DNA-methyltransferase (adenine-specific) dam methylase gene product [Vibrio cholerae]	4.0
187	AF005638	Tupaia glis apolipoprotein AI prepropeptide mRNA, complete cds	1.7	3355682	(AL031124) putative secreted lyase	4.0
188	M23090	Human germline IgK chain gene V3-region, clone Humkv328h5	1.7	2257483	(AB004534) pi003 [Schizosaccharomyces pombe]	4.0
189	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.7	2143504	myotonic dystrophy kinase - mouse (fragment) kinase, DM-kinase {C-terminal, alternatively spliced, clone delta II.III.IV.V} [mice, brain, Peptide Partial, 474 aa] [Mus sp.]	3.9
190	X59964	H.sapiens CST4 gene for Cystatin D	1.7	1766075	(U37273) winged helix protein CWH-2 [Gallus gallus]	3.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					HYPOTHETICAL 11.7 KB	
191	X95276	<i>P. falciparum</i> complete gene map of plastid-like DNA (IR-B)	1.7	3219951	PROTEIN C6B12.13 IN CHROMOSOME I >gi 2330843 gnl PID e334047 pombe]	3.0
192	D84487	Rat PMSG-induced ovarian mRNA, 3' sequence, N10	1.7	173164	(J02719) valyl-tRNA synthetase [<i>Saccharomyces cerevisiae</i>]	2.3
193	L14851	<i>Rattus norvegicus</i> neurexin III-alpha gene, complete cds.	1.7	3323586	(AF060869) single-strand binding protein [<i>Salmonella typhimurium</i>]	2.3
194	M97002	<i>Xenopus laevis</i> /gilli hybrid pseudo-IgH chain gene, V region, clone LG7G342A.	1.7	2118407	MHC sex-limited protein - mouse (fragment) musculus]	2.3
195	L07025	<i>Bacillus thuringiensis</i> delta-endotoxin (CryA(a)) gene, 5' end. > :: gb I34520 I34520 Sequence 1 from patent US 5596071 > :: gb I39790 I39790 Sequence 1 from patent US 5616495 > :: gb AR008487 AR008487 Sequence 1 from patent US 5753492	1.7	2496940	HYPOTHETICAL 53.4 KD PROTEIN D1054.13 IN CHROMOSOME V >gi 3875316 gnl PID e1344967	1.8
196	S73149	insulin-like growth factor II {intron 7} [human, Genomic, 1702 nt]	1.7	3327038	(AB014512) KIAA0612 protein [Homo sapiens]	1.8
197	D86990	Human (lambda) DNA for immunoglobulin light chain	1.7	494367	Fv Fragment (Murine Se155-4) Complex With The Trisaccharide: Alpha-D-Galactose(1-2)[alpha-D-Abequose(1-3)]alpha-D-Mannose (P1-Ome) (Part Of The Cell-Surface Carbohydrate Of Pathogenic Salmonella)	1.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
198	L17027	Plasmid pFdA (from <i>Fremyella diplosiphon</i>) DNA sequence, including unidentified cds and stem loop.	1.7	1082702	poliovirus receptor-related protein - human	1.4
199	AL022273	<i>Caenorhabditis elegans</i> cosmid H22D14, complete sequence [<i>Caenorhabditis elegans</i>]	1.7	3924605	(AF069442) putative inhibitor of apoptosis [<i>Arabidopsis thaliana</i>]	1.4
200	U89926	<i>Drosophila melanogaster</i> cut gene, partial sequence	1.7	2245100	(Z97343) DNA-binding protein homolog	1.3
201	Z25749	H.sapiens gene for ribosomal protein S7	1.7	2493459	PROTEIN KINASE C SUBSTRATE, 60.1 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN) >gi1215746	1.1
202	U59841	<i>Fundulus heteroclitus</i> lactate dehydrogenase B	1.7	3005587	(AF048977) Ser/Arg-related nuclear matrix protein [<i>Homo sapiens</i>]	0.82
203	X55763	Rabbit mRNA for smooth muscle calcium channel blocker (CaCB) receptor	1.7	3883128	(AF082302) arabinogalactan-protein [<i>Arabidopsis thaliana</i>]	0.82
204	Z75528	<i>Caenorhabditis elegans</i> cosmid C18B12A, complete sequence [<i>Caenorhabditis elegans</i>]	1.7	940397	(D10123) core [Hepatitis C virus]	0.80
205	U50912	Human XIST gene, poly purine-pyrimidine repeat region	1.7	2338027	(AF005370) large tegument protein [<i>Alcelaphine herpesvirus 1</i>]	0.59
206	X12817	<i>Ovis aries</i> beta-lactoglobulin gene	1.7	987050	(X65335) lacZ gene product (unidentified cloning vector)	0.45
207	AF004419	<i>Homo sapiens</i> troponin T (TNNT2) gene, exon 13	1.7	2996364	(AF053947) unknown [<i>Yersinia pestis</i>] >gi3883090	0.22
208	L43643	<i>Gallus domesticus</i> DNA microsatellite marker MCW119	1.7	464896	TRANSDUCIN-LIKE ENHANCER PROTEIN 1 enhancer-of-split homolog TLE-1 - human >gi307510	0.20

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
209	Z73278	<i>S.cerevisiae</i> chromosome XII reading frame ORF YLR106c	1.7	1351657	HYPOTHETICAL 123.9 KD PROTEIN C30D11.04C IN CHROMOSOME I >gi 2130411 pir S62562 hypothetical protein SPAC30D11.4c - fission yeast nuclear pore complex protein [Schizosaccharomyces pombe]	0.20
210	M22345	Mouse endogenous provirus gag, pol, and env region DNA.	1.7	2444455	(AF020765) hypothetical protein [Myxococcus xanthus]	0.12
211	AE000360	<i>Escherichia coli</i> K-12 MG1655 section 250 of 400 of the complete genome	1.7	2736361	(AF039038) No definition line found [Caenorhabditis elegans]	0.12
212	AB020692	Homo sapiens mRNA for KIAA0885 protein, complete cds	1.7	2605924	(AF029726) histidine kinase C [Dictyostelium discoideum]	0.094
213	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.092
214	S69429	testis-determining gene/SRY homolog [Sminthopsis macroura=striped-faced dunnarts, Genomic, 855 nt]	1.7	2499016	TONB PROTEIN >gi 1666536 (U23764) TonB [Pseudomonas aeruginosa]	0.088
215	U67205	Mus musculus ACF7 neural isoform 3 (mACF7) mRNA, partial cds	1.7	2047349	(AF000198) weak similarity to HSP90 [Caenorhabditis elegans]	0.052
216	X98188	Artificial DNA sequence for mammalian lambda-neo minichromosome, 1400 bp	1.7	2493779	PUTATIVE CUTICLE COLLAGEN C09G5.6 collagen: cDNA EST yk244c3.5 comes from this gene; cDNA EST yk244c3.3 comes from this gene [Caenorhabditis elegans]	0.042
217	U70139	Mus musculus putative CCR4 protein mRNA, partial cds	1.7	2252630	(U95973) hypothetical protein [Arabidopsis thaliana]	0.041

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
218	L38808	Homo sapiens alpha-1 type V collagen (COL5A1) gene, 5' flank and exon 1.	1.7	2895760	(AF045246) universal minicircle sequence binding protein minicircle sequence binding protein [Crithidia fasciculata]	0.039
219	Z72151	B.napus mRNA for AMP-binding protein	1.7	190475	(K02576) salivary proline-rich protein 1 [Homo sapiens]	0.011
220	X94152	R.norvegicus mRNA for cysteine sulfinate decarboxylase	1.7	2136212	synapsin IIb - human >gi1594277 (U40215) synapsin IIb [Homo sapiens]	0.008
221	L20255	Mouse stathmin gene sequence.	1.7	2317934	(U97553) unknown [murine herpesvirus 68]	0.006
222	L13600	Rattus norvegicus glycine transporter mRNA, complete cds.	1.7	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	0.003
223	AJ224150	Plasmodium berghei EF-1alpha A-gene	1.7	2072290	(U95094) XL-INCENP [Xenopus laevis]	0.001
224	S80642	butyrophilin [mice, lactating mammary gland, mRNA Partial, 3193 nt]	1.7	2695746	(AJ223010) Pmt2 [Schizosaccharomyces pombe]	9e-04
225	M22363	C.elegans unc-86 gene encoding two alternative proteins, complete cds.	1.7	2224683	(AB002369) KIAA0371 [Homo sapiens]	1e-04
226	X92123	M.musculus cgt gene exon 1	1.7	3874232	(Z49909) similar to Prokaryotic ribonuclease PH [Caenorhabditis elegans]	3e-05
227	AB016000	Ipomoea nil Pkn2 (knotted-like gene) mRNA, complete cds	1.7	2183083	(AF000422) TTF-I interacting peptide 5 [Homo sapiens]	1e-05
228	D14133	Bovine mRNA for synaptocanalin I	1.7	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	2e-06

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
229	L01991	Mus musculus TAFG-1-like neuronal glycoprotein (PCS) mRNA, complete cds.	1.7	3006139	(AL022299) hypothetical protein	4e-07
230	X63016	Tomato yellow leaf curl virus Thailand isolate complete genome (TYLCV-TH B-DNA)	1.7	3643608	(AC005395) hypothetical protein [Arabidopsis thaliana]	1e-07
231	Z22802	H.sapiens microsatellite repeat. > :: gb G34562 G34562 human STS SHGC-51834	1.7	100210	extensin precursor (clone Tom L 4) - tomato esculentum]	4e-09
232	K02765	Human complement component C3 mRNA, alpha and beta subunits, complete cds.	1.7	2984320	(AE000773) acetoin utilization protein [Aquifex aeolicus]	1e-09
233	Z74818	S.cerevisiae chromosome XV reading frame ORF YOL076w	1.7	3873700	(Z73102) predicted using Genefinder; Similarity to Bacillus subtilis DNAJ protein gene; cDNA EST EMBL:C12520 comes from this gene; cDNA EST EMBL:D71409 comes from this ge...	7e-11
234	D21871	Pig mRNA for thimet oligopeptidase	1.7	2632098	(Y15513) Prodos protein [Drosophila melanogaster]	8e-13
235	Y14344	Gallus gallus gene encoding neurofascin, exons 9,10,11 & 12	1.7	3876421	(Z81070) cDNA EST EMBL:C12730 comes from this gene; cDNA EST yk200b6.5 comes from this gene; cDNA EST yk349a12.5 comes from this gene [Caenorhabditis elegans]	3e-14
236	Z73608	S.cerevisiae chromosome XVI reading frame ORF YPL252c	1.7	1439663	(U64605) C05D9.6 gene product [Caenorhabditis elegans]	6e-18

Nearest Neighbor (BlastN vs. Genbank)				Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					OLIGOSACCHARYL	
237	AG000518	Homo sapiens genomic DNA, 21q region, clone: T171N23	1.7	1174468	TRANSFERASE STT3 SUBUNIT HOMOLOG >gi 529357 (U13019) No definition line found [Caenorhabditis elegans]	6e-18
238	D17716	Human mRNA for N-acetylglucosaminyltransferase V, complete cds	1.7	961446	(D63877) KIAA0157 gene product is novel.	5e-19
239	AF102512	Cheilodactylus vittatus country USA: Midway Island cytochrome c oxidase subunit I gene, mitochondrial gene encoding mitochondrial protein, partial cds	1.7	1572756	(U70848) C43G2.1 gene product [Caenorhabditis elegans]	5e-40
240	L30107	Rattus norvegicus liver-specific transporter gene, promoter region.	1.7	4176443	(AL022238) dJ1042K10.4 (novel protein)	3e-49
241	X91220	H.sapiens mRNA for Na-Cl electroneutral thiazide-sensitive cotransporter	1.7	3478637	(AC005546) R29425_1 [Homo sapiens]	6e-54
242	U97146	Rattus norvegicus calcium-independent phospholipase A2 mRNA, complete cds	1.6	<NONE>	<NONE>	<NONE>
243	Z48508	Pea seed-borne mosaic virus RNA for coat protein and polymerase (partial)	1.6	<NONE>	<NONE>	<NONE>
244	M18349	Rat leukocyte common antigen (L-CA) gene, exons 1 through 5.	1.6	<NONE>	<NONE>	<NONE>
245	M13158	Yeast (S.pombe) cdc25+ gene (mitosis initiation), complete cds.	1.6	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mycoplasma				
246	U39712	genitalium section 34 of 51 of the complete genome	1.6	<NONE>	<NONE>	<NONE>
247	M17922	Mouse Murine urokinase-type plasminogen activator protein gene, complete cds.	1.6	3875750	(Z81499) predicted using Genefinder; cDNA EST yk410e3.3 comes from this gene; cDNA EST yk410e3.5 comes from this gene [Caenorhabditis elegans]	8.0
248	M89986	Human polymorphic loci in Xq28.	1.6	3261710	(Z84724) psd [Mycobacterium tuberculosis]	6.4
249	M89986	Human polymorphic loci in Xq28.	1.6	2143805	inositol-polyphosphate 4-phosphatase - rat	6.2
250	U68725	Rattus norvegicus Deleted in colorectal Cancer	1.6	1256804	(U51449) RING3 protein [Xenopus laevis]	5.8
251	X95199	P.platessa GSTA, GSTA1, GSTA2, and PPTN genes	1.6	3915113	MALEYLACETATE REDUCTASE Pseudomonas cepacia >gi 643636 (U19883) maleylacetate reductase [Burkholderia cepacia]	4.9
252	Y09103	D.melanogaster RPA1 gene	1.6	3916021	HYPOTHETICAL 91 KD PROTEIN IN COB INTRON >gi 2654230 gnl PID e1192341 (X02819) unidentified reading frame [Schizosaccharomyces pombe]	4.8
253	Z14078	T.aestivum mitochondrion fMet, 18S, 5S repeat unit DNA	1.6	2501668	DYSTROPHIN-RELATED PROTEIN 2 sapiens]	3.6
254	AB002314	Human mRNA for KIAA0316 gene, complete cds	1.6	130997	REPETITIVE PROLINE-RICH CELL WALL PROTEIN 1 PRECURSOR >gi 81809 pir A29324 proline-rich protein precursor - soybean >gi 170049 (J02746) proline-rich protein [Glycine max]	2.8
255	M21488	Human muscle creatine kinase gene (CKMM), exon 2.	1.6	119399	ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: COAT PROTEIN GP62; COAT PROTEIN GP40]	2.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
256	AE001164	<i>Borrelia burgdorferi</i> (section 50 of 70) of the complete genome	1.6	4050089	(AF109907) hypothetical protein [Homo sapiens]	1.5
257	X61757	<i>M.musculus</i> rearranged T-cell receptor beta variable region (Vb17a)	1.6	3377766	(AF080090) semaphorin IV isoform b [Mus musculus]	1.2
258	M15346	<i>T.cruzi</i> tandemly repeated gene encoding an 85 kDa antigen with homology to heat shock proteins.	1.6	2804437	(AF043695) similar to zinc metalloprotease family of peptidases [Caenorhabditis elegans]	0.41
259	L39018	<i>Rattus norvegicus</i> sodium channel protein 6 (SCP6) mRNA, complete cds	1.6	2920535	(AF018081) type XVIII collagen [Homo sapiens]	0.037
260	M29483	Human leukocyte adhesion protein p150.95 alpha subunit gene, exons 7 - 15.	1.6	1840045	(U49082) transporter protein [Homo sapiens]	2e-09
261	L06844	<i>Aspergillus niger</i> beta D-fructofuranosidase (suc1) gene, one exon.	1.6	4206210	(AF071527) putative calcium channel [Arabidopsis thaliana]	9e-10
262	M10946	Chicken aldolase B gene, complete cds, clones lambda-C(11.1.4).	1.6	2746775	(AF040640) similar to peptidase family C19 (ubiquitin carboxyl-terminal hydrolase) [Caenorhabditis elegans]	1e-31
263	X07881	Human gene PRB3L for proline-rich protein G1	1.5	<NONE>	<NONE>	<NONE>
264	U22260	<i>Nicotiana tabacum</i> UMP synthase (pyr5-6) mRNA, partial cds	1.5	3880923	(Z99271) similar to Reverse transcriptase comes from this gene [Caenorhabditis elegans]	0.50
265	U76759	<i>Mus musculus</i> nuclear protein NIP45 mRNA, complete cds	1.4	1330394	(U58761) C01F1.6 gene product [Caenorhabditis elegans]	8.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
266	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	1.4	1703461	POTASSIUM-TRANSPORTING ATPASE BETA CHAIN (PROTON PUMP) (GASTRIC H ⁺ /K ⁺ ATPASE BETA SUBUNIT) 3.6.1.36) beta chain - human >gi 184105 (M75110) H,K-ATPase beta subunit [Homo sapiens]	8.9
267	X64659	C.jacchus interferon gene for interferon gamma	1.4	1486485	(U28832) US10 [Gallid herpesvirus 1] >gi 1486497	6.8
268	U11825	Schistosoma japonicum structural muscle protein paramyosin mRNA, complete cds.	0.88	<NONE>	<NONE>	<NONE>
269	D84278	Human DNA for CD38, exon 1	0.68	3766363	(AL031907) hypothetical serine rich protein [Schizosaccharomyces pombe]	3.0
270	M59755	Bovine lens aldose reductase pseudogene, 3' end.	0.67	<NONE>	<NONE>	<NONE>
271	M81758	Homo sapiens skeletal muscle voltage-dependent sodium channel alpha subunit (SkM1) mRNA, complete cds.	0.65	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.6
272	L01965	Human type IV sodium channel alpha polypeptide	0.64	2437819	(Z86105) 1,4-beta-glucanase [Anaerocellum thermophilum]	3.5
273	U90122	Danio rerio bone morphogenetic protein-4 (bmp4) mRNA, partial cds	0.63	2983532	(AE000720) formate dehydrogenase alpha subunit [Aquifex aeolicus]	7.9
274	L41624	Hylobates lar mucin (MUC1) gene, exons 1-6.	0.63	1517808	(D79215) FGF-10 [Rattus norvegicus]	0.91

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
275	AF030881	Fugu rubripes sushi retrotransposon gag polyprotein (gag) and pol polyprotein (pol) genes, complete cds	0.63	1519696	(U67956) coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.3; coded for by C. elegans cDNA yk126f9.3; coded for by C. elegans cDNA yk159h6.5 [Caenorhabditis elegans]	0.38
276	U52909	Arabidopsis thaliana U1 snRNP 70K protein gene, complete cds	0.62	<NONE>	<NONE>	<NONE>
277	AF008192	Homo sapiens putative GR6 protein (GR6) mRNA, complete cds	0.62	3800934	(AF100655) contains similarity to scr/thr protein kinases [Caenorhabditis elegans]	9.7
278	U17081	Human fatty acid binding protein (FABP3) gene, complete cds	0.62	3617848	(AF049709) tyrosylprotein sulfotransferase-A; TPST-A	7.7
279	AB018340	Homo sapiens mRNA for KIAA0797 protein, partial cds	0.62	424044	VP5 protein - porcine rotavirus >gi 61355	7.7
280	Y00093	H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.62	1054945	(U38621) polypeptide [Tobacco vein mottling virus]	4.5
281	M63138	Human cathepsin D (catD) gene, exons 7, 8, and 9.	0.62	136810	GLYCOPROTEIN M >gi 73791 pir WMBE51 UL10 protein - human herpesvirus 1 1-473 [Human herpesvirus 1] >gi 221732 gnl PID d1002131	3.5
282	X76056	N. sylvestris DNA for spacer region between 25S and 18S ribosomal RNA genes	0.62	2661176	(U76671) putative cds [Rhodobacter sphaeroides]	2.0
283	X74501	B.taurus mRNA for ACTH receptor	0.62	4249552	(AB001075) galectin-2 related protein	2.0
284	M57634	Rat F1-ATPase beta subunit mRNA, 3' end.	0.62	2119692	transforming growth factor-beta type III receptor - chicken >gi 511843 (L01121) transforming growth factor-beta type III receptor [Gallus gallus]	1.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
285	Y15724	Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	0.62	2498164	ASPARTYL/ASPARAGINYL BETA-HYDROXYLASE (ASPARTATE BETA-HYDROXYLASE) (ASP BETA-HYDROXYLASE) (PEPTIDE-ASPARTATE BETA-DIOXYGENASE) beta-dioxygenase (EC 1.14.11.16) - bovine >gi 162694 taurus]	0.52
286	AL010142	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence	0.62	3183206	HYPOTHETICAL PROTEIN KIAA0009 sapiens]	4e-07
287	AB008160	Mus musculus Stat3 gene, 5'-flanking region and exon 1 partial sequence	0.62	466097	HYPOTHETICAL 63.5 KD PROTEIN ZK353.1 IN CHROMOSOME III >gi 1078903 pir S44654 ZK353.1 protein - Caenorhabditis elegans >gi 289757 (L15313) putative [Caenorhabditis elegans] (Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4...	1e-35
288	AB018795	Halomonas marina gene for alginate lyase, complete cds	0.62	3877493		3e-46
289	Z69906	Human DNA sequence from cosmid E141E2, on chromosome 22, complete sequence [Homo sapiens]	0.61	<NONE>	<NONE>	<NONE>
290	U18259	Human clone CIITA-8 MHC class II transactivator CIITA mRNA, complete cds.	0.61	1483567	(X79983) viral proteinase [Pseudorabies virus]	9.8
291	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.61	475724	(U08884) protein VIII precursor [Bovine adenovirus type 3]	7.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
292	U70825	Rattus norvegicus 5-oxo-L-prolinase mRNA, complete cds	0.61	733543	(U23448) similar to genome polypeptide (SP:POLG_BVDVN, P19711); alternative splicing to C04A2.7a	4.4
293	L81667	Homo sapiens (subclone 2_a9 from P1 H49) DNA sequence	0.61	2565087	(U80759) CAGH4 alternate open reading frame [Homo sapiens]	3.3
294	AE000760	Aquifex aeolicus section 92 of 109 of the complete genome	0.61	2811092	HOMEBOX PROTEIN HOX-A3 (HOX-1.5) homeobox-containing transcription factor [Mus musculus]	2.6
295	U58512	Mus musculus Rho-associated, coiled-coil forming protein kinase p160 ROCK-1 mRNA, complete cds	0.61	295671	(L11275) selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III	1.5
296	U27459	Human origin recognition complex protein 2 homolog hORC2L mRNA, complete cds	0.61	200285	(M97900) putative open reading frame [Mus musculus]	0.66
297	L36680	Pisum sativum S-adenosylmethionine synthase mRNA, 3' end.	0.61	2285790	(AB002086) p47 [Rattus norvegicus]	4e-12
298	AE000673	Aquifex aeolicus section 5 of 109 of the complete genome	0.61	3395782	(AF058446) histone macroH2A1.2 [Gallus gallus]	6e-27
299	AF086310	Homo sapiens full length insert cDNA clone ZD51F08	0.61	3646450	(AL031603) conserved hypothetical protein. [Schizosaccharomyces pombe]	8e-29
300	AJ009675	Agrotis ipsilon mRNA for 3-hydroxy-3-methylglutaryl coenzyme A reductase	0.61	4176370	(AC005058) similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	2e-73
301	AC005577	Homo sapiens chromosome 19, cosmid F18382B, centromeric end, complete sequence [Homo sapiens]	0.60	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Candida albicans				
302	U40454	topoisomerase type I (CATOP1) gene, complete cds	0.60	<NONE>	<NONE>	<NONE>
303	J01390	Emericella nidulans mtDNA between h2/h5 and bh2/b2 junctions. genes for ATPase subunit 6, cytochrome oxidase subunit 3, seven. unidentified proteins, twentyfour tRNA's and L-rRNA.	0.60	<NONE>	<NONE>	<NONE>
304	L11172	Plasmodium falciparum RNA polymerase I gene, complete cds.	0.60	<NONE>	<NONE>	<NONE>
305	Z81079	Caenorhabditis elegans cosmid F39H11, complete sequence [Caenorhabditis elegans]	0.60	<NONE>	<NONE>	<NONE>
306	Z49627	S.cerevisiae chromosome X reading frame ORF YJR127c	0.60	118751	MAJOR DNA-BINDING PROTEIN herpesvirus 1 (strain 11) >gi 60327 (X64346) major ssDNA-binding protein [Saimiriine herpesvirus 2]	9.6
307	U94911	Rattus norvegicus H-K-ATPase alpha 2 gene, alternatively spliced products and partial cds	0.60	2213862	(AF003086) PfsNF2L [Plasmodium falciparum]	7.4
308	U67476	Methanococcus jannaschii section 18 of 150 of the complete genome	0.60	1749688	(D89240) unnamed protein product	5.7
309	U67513	Methanococcus jannaschii section 55 of 150 of the complete genome	0.60	3327421	(U97068) zonadhesin [Mus musculus]	4.3
310	U57817	Haemophilus ducreyi lipoprotein gene, complete cds	0.60	4008577	(AL034491) conserved hypothetical protein [Schizosaccharomyces pombe]	2.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					probable protein-tyrosine kinase (EC 2.7.1.112) RTK - Pacific electric ray >gi290858	1.5
311	X80700	H.sapiens G17 gene	0.60	422541		
312	L42167	Mus musculus (clone R24) rds gene, partial cds	0.60	4220848	(AF033823) moira [Drosophila melanogaster]	0.51
313	U54777	Human hMSH6 mRNA, complete cds	0.60	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07
314	D86985	Human mRNA for KIAA0232 gene, complete cds	0.60	1938462	(U97006) No definition line found [Caenorhabditis elegans] (U55376) coded for by C. elegans cDNA cm21e6; coded for by C. elegans cDNA cm01e2; similar to melibiose carrier protein (thiomethylgalactoside permease II)	2e-07
315	D43964	Rat liver mRNA for Kan-1, complete cds	0.60	1280135		5e-15
316	U49058	Rattus norvegicus CTD-binding SR-like protein RA4 mRNA, partial cds	0.60	2145091	(U37500) RNA polymerase II largest subunit [Mus musculus]	1e-19
317	X84388	U.ruddi mitochondrial 12S ribosomal RNA	0.60	3874247	(Z70205) predicted using Genefinder	2e-37
318	AF125447	Caenorhabditis elegans cosmid Y14H12B	0.59	<NONE>	<NONE>	<NONE>
319	U20189	Hyoscyamus muticus clone cVS2 vetispiradiene synthase mRNA, partial cds.	0.59	<NONE>	<NONE>	<NONE>
320	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete cds.	0.59	<NONE>	<NONE>	<NONE>
321	AJ132366	Helicobacter pylori (strain P1) comB and pmf/algA (partial) genes, and partial ORF1 and ORF2	0.59	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
322	U17289	transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.59	2459419	(AC002332) hypothetical protein [Arabidopsis thaliana]	9.4
323	Z71466	S.cerevisiae chromosome XIV reading frame ORF YNL190w	0.59	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	7.3
324	Z66493	Beet soil-borne virus genes for 13K, 22K and 48K proteins	0.59	2119867	cryV465 protein - Bacillus thuringiensis thuringiensis]	7.2
325	L41351	Homo sapiens prostasin mRNA, complete cds	0.59	729212	CRYSTALLIN J1C crystallin [Tripedalia cystophora]	4.2
326	X79854	S.lincolnensis gene for 16S ribosomal RNA	0.59	3702828	(AF056577) high mobility group protein 1.2	3.2
327	AJ223356	Strongylocentrotus purpuratus mRNA for SuDp98 protein	0.59	2495704	HYPOTHETICAL PROTEIN KIAA0129 product is novel. [Homo sapiens]	2.5
328	X86019	H.sapiens mRNA for PRPL-2 protein	0.59	1743341	(Y10027) transcription factor TEF-1 [Mus musculus]	2.5
329	U75528	Xiphias gladius creatine kinase gene, partial cds	0.59	1845995	(U69477) envelope glycoprotein [Human immunodeficiency virus type 1]	2.4
330	AC005573	Homo sapiens chromosome 5, PAC clone 202e13	0.59	2506366	DNA POLYMERASE EPSILON SUBUNIT B DNA-directed DNA polymerase (EC 2.7.7.7) II chain B - yeast. (Saccharomyces cerevisiae) >gi 786319 (U25842) DNA Polymerase epsilon, subunit B (Swiss Prot. accession number P24482) [Saccharomyces cerevisiae]	1.4
331	L19180	Rat receptor-linked protein tyrosine phosphatase	0.59	1235974	(X96713) collagen [Globodera pallida]	1.1
332	L32090	Listeria monocytogenes secA gene, complete cds.	0.59	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.83

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
333	U24433	Xenopus laevis syndecan-2 mRNA, complete cds.	0.59	3355692	(AL031124) hypothetical protein SC1C2.25c [Streptomyces coelicolor]	0.64
334	M23412	Drosophila muscarinic acetylcholine receptor mRNA, complete cds.	0.59	168237	(M76546) hydroxyproline-rich protein [Helianthus annuus]	0.22
335	AF060729	Synaphea media chloroplast atpB-rbcL intergenic spacer region, partial sequence	0.59	731596	HYPOTHETICAL 67.5 KD PROTEIN IN PRPS4-STE20 INTERGENIC REGION >gi 626567 pir S46825 hypothetical protein YHL010c - yeast (Saccharomyces cerevisiae) >gi 2289881 (U11582) No definition line found [Saccharomyces cerevisiae]	0.16
336	AF029734	Xanthobacter autotrophicus transcriptional activator AldR (aldR) gene, partial cds; and NAD-dependent chloroacetaldehyde dehydrogenase (aldB) gene, complete cds	0.59	2498801	PERIAXIN >gi 2143901 pir I58157 periaxin - rat >gi 505297 (Z29649) periaxin [Rattus norvegicus]	0.13
337	X95307	C.reinhardtii LI818r- 1 gene	0.59	1723781	HYPOTHETICAL 34.3 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION >gi 2131717 pir S64612 hypothetical protein YGR277c - yeast (Saccharomyces cerevisiae) >gi 1323505 gnl PID e243248 (Z73062) ORF YGR277c [Saccharomyces cerevisiae]	1e-04
338	M24572	Dictyostelium discoideum tRNA- Glu-GAA gene, clone yGluGAA.8.	0.59	1176186	HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DACB-RPMA INTERGENIC REGION >gi 606121 coli]	3e-06
339	U73733	Human hMSH6 gene, exon 2	0.59	2665637	(AF031087) mismatch repair protein MSH6 [Mus musculus]	5e-07

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Escherichia coli				
340	D90747	genomic DNA. (25.2-25.6 min)	0.59	134286	DOLICHOL KINASE	6e-08
341	J05211	Human desmoplakin mRNA, 3' end.	0.59	246796	major centromere protein, CENP-B [human, Peptide, 594 aa]	4e-08
342	L24441	Loligo pealii kinesin light chain mRNA, complete cds.	0.59	547800	KINESIN LIGHT CHAIN (KLC) sea urchin (Strongylocentrotus purpuratus) >gil161530	5e-14
343	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.58	<NONE>	<NONE>	<NONE>
344	L81932	Homo sapiens (subclone 9_h2 from P1 H21) DNA sequence	0.58	<NONE>	<NONE>	<NONE>
345	AF087966	Homo sapiens full length insert cDNA clone YU51G04	0.58	<NONE>	<NONE>	<NONE>
346	Z78574	H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10G11	0.58	<NONE>	<NONE>	<NONE>
347	AF068061	Blattella germanica allatostatin neuropeptide precursor, gene, complete cds	0.58	<NONE>	<NONE>	<NONE>
348	AF015592	Homo sapiens Cdc7 (CDC7) mRNA, complete cds	0.58	<NONE>	<NONE>	<NONE>
349	AF028006	Methanosarcina barkeri atp operon: ATP synthase beta subunit (atpD), ATP synthase epsilon subunit (atpC), ATP synthase gene I (atpI), ATP synthase a subunit subunit (...)	0.58	3184291	(AC004136) putative DNA polymerase III gamma subunit	9.4
350	AB017032	Mus musculus gene for pancreatic trypsin, complete cds	0.58	3170561	(AF056704) synapsin IIIa [Rattus norvegicus]	9.2

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Dictyostelium discoideum developmental protein DG1110 (DG1110) gene, partial cds				
351	AF081585		0.58	105417	basic proline-rich peptide IB-8a human	9.2
352	AF086322	Homo sapiens full length insert cDNA clone ZD53E01	0.58	93026	hypothetical protein - African swine fever virus (strain Malawi Lil-20/1) >gi 450758 (X71982) myeloid differentiation antigen homologue [African swine fever virus] >gi 903686 (M95672) unknown protein	7.1
353	AF088025	Homo sapiens full length insert cDNA clone ZC19C04	0.58	2384644	(U92805) thrombospondin-3 [Xenopus laevis]	7.0
354	AB002339	Human mRNA for KIAA0341 gene, partial cds	0.58	2135587	M130 antigen (cytosolic variant 2) - human	5.4
355	U67548	Methanococcus jannaschii section 90 of 150 of the complete genome	0.58	2911094	(AL021957) hypothetical protein Rv2174	4.2
356	L07868	Homo sapiens receptor tyrosine kinase (ERBB4) gene, complete cds.	0.58	461922	PYRUVATE DECARBOXYLASE (8-10 NM CYTOPLASMIC FILAMENT-ASSOCIATED PROTEIN) (P59NC) 4.1.1.1) - Neurospora crassa >gi 293948 (L09125) pyruvate decarboxylase [Neurospora crassa] >gi 1655909	4.2
357	X03897	Bacillus subtilis sigma 43 operon with P23-dnaE-rpoD genes (dnaE for DNA primase, rpoD for RNA polymerase)	0.58	1323704	(U55387) similar to C. elegans F38E1.9 gene product encoded by GenBank Accession Number U41996 [Cricetulus griseus]	4.1
358	D76419	Desulfovibrio vulgaris rbo gene for desulfoferredoxin and rub gene for rubredoxin, complete cds	0.58	3420047	(AC004680) putative protein kinase [Arabidopsis thaliana]	2.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human DNA				
359	Z82174	sequence from cosmid B20F6 on chromosome 22, complete sequence [Homo sapiens]	0.58	2145455	(Y07866) catalase-peroxidase	2.4
360	M33642	F.solani STI35 protein gene, complete cds.	0.58	2896706	(AL021897) hypothetical protein Rv1069c	2.4
361	U64873	Mus musculus transforming growth factor alpha (TGF alpha) gene, partial cds	0.58	3874437	(Z81038) predicted using Genefinder; cDNA EST yk488a2.5 comes from this gene [Caenorhabditis elegans]	1.8
362	AB002132	Macrophthalmus banzai mitochondrial DNA for 12S and 16S rRNA, partial and complete sequence	0.58	2960022	(AJ224676) rho type GEF [Drosophila melanogaster]	1.8
363	AF070070	Caenorhabditis elegans MutS homolog (msh-5) mRNA, partial cds	0.58	4098205	(U75869) Omp22 [Helicobacter pylori]	1.8
364	AF045240	Staphylococcus epidermidis plasmid pIP1629 mobilization protein (mobC1), (orf69-1), (mobA1),	0.58	4218117	(AL035353) protein (fragment)	0.62
365	X61637	H.sapiens Wilms tumor gene 1, exons 8 and 9	0.58	2331059	(U88211) unknown [Gallus gallus]	0.62
366	AF039312	Moraxella catarrhalis strain 4223 transferrin binding protein A (tbpA) and transferrin binding protein B (tbpB) genes, complete cds; and unknown gene	0.58	120155	FIBER PROTEIN >gi 74229 pir ERADFM fiber protein - mouse adenovirus 1 >gi 209758 (M30594) fiber protein [Mastadenovirus mus1]	0.27
367	D87463	Human mRNA for KIAA0273 gene, complete cds	0.58	3861477	(U94177) androgen receptor [Pan troglodytes]	0.12
368	U40342	Mus musculus ninein mRNA, complete cds.	0.58	4115936	(AF118223) No definition line found [Arabidopsis thaliana]	0.004

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
369	S57235	CD68=110kda transmembrane glycoprotein (human, promonocyte cell line U937, mRNA, 1722 nt)	0.58	2072501	(U96113) WWP1 [Homo sapiens]	1e-04
370	U39391	Mus musculus serotonin1A receptor mRNA, complete cds.	0.58	1469876	(D63481) The KIAA0147 gene product is related to adenylyl cyclase. [Homo sapiens]	1e-07
371	D00056	Monkey B-lymphotropic papovavirus genes for VP-1, 2, 3 and large T antigen, complete and partial cds, strain LPV-76 > :: gb M14494 PPMVP1 M Monkey B-lymphotropic papovavirus mutant (LPV-76) PstI B fragment encoding VP1, VP2, VP3 and T-antigen.	0.58	2462069	(AJ001774) vanadium chloroperoxidase	1e-08
372	M77182	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. > :: gb I16670 I16670 Sequence 1 from patent US 5476781	0.58	1730722	HYPOTHETICAL 43.8 KD PROTEIN IN NCE3-HHT2 INTERGENIC REGION >gi 2131871 pir S62957 hypothetical protein YNL035c - yeast (Saccharomyces cerevisiae) >gi 1301880 gnl PID e239670 (Z71311) ORF YNL035c [Saccharomyces cerevisiae]	8e-14
373	S72579	igloo-S=growth-associated protein GAP-43 homolog	0.58	2689720	(AF037168) DnaJ homologue [Arabidopsis thaliana]	7e-14
374	AF018165	Tetraodon fluviatilis amyloid precursor protein mRNA, complete cds	0.58	3219938	HYPOTHETICAL 34.9 KD PROTEIN C57A10.11C IN CHROMOSOME I >gi 2058378 gnl PID e314002 [pombe]	5e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
375	U81803	Filobasidiella neoformans translation elongation factor EF1-alpha (CnTEF1) mRNA, complete cds	0.57	<NONE>	<NONE>	<NONE>
376	U09781	Candida albicans ATCC 18804, CBS 562 peptide transporter gene, complete cds.	0.57	<NONE>	<NONE>	<NONE>
377	AC002143	Homo sapiens (subclone 4_b10 from BAC H102) DNA sequence	0.57	<NONE>	<NONE>	<NONE>
378	U23442	Tetrahymena thermophila RR internal deletion sequence.	0.57	<NONE>	<NONE>	<NONE>
379	U17289	Mus musculus transcription factor AP-2 (AP-2) gene, alternative exon 1a, and isoform 2, partial cds.	0.57	<NONE>	<NONE>	<NONE>
380	X70844	Buzura suppressaria nuclear polyhedrosis virus gene for polyhedrin protein	0.57	<NONE>	<NONE>	<NONE>
381	AJ012159	Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene	0.57	<NONE>	<NONE>	<NONE>
382	X76571	H.sapiens simple DNA sequence region clone wg1a8.	0.57	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
383	AF034434	Vibrio cholerae pathogenicity island, putative transposase, aldehyde dehydrogenase (aldA), toxR-activated gene A protein (tagA), putative inner membrane protein, and putative zinc metalloprotease genes, complete cds; and...	0.57	<NONE>	<NONE>	<NONE>
384	AB017031	Mus musculus gene for TESP4, complete cds	0.57	<NONE>	<NONE>	<NONE>
385	X89788	S.hispidus mitochondrial DNA for SSU ribosomal RNA gene	0.57	<NONE>	<NONE>	<NONE>
386	L16921	Rat progesteron receptor gene, 5' untranslated region.	0.57	3323116	(AE001251) femA protein, putative [Treponema pallidum]	8.9
387	AF027292	Homo sapiens interferon regulatory factor 6	0.57	259790	(S48157) DNA polymerase-primase 180 kda subunit [Drosophila melanogaster. Peptide, 1490 aa]	6.7
388	AJ012581	Cicer arietinum mRNA for cytochrome P450	0.57	2131498	hypothetical protein YDR446w - yeast CAI: 0.11 [Saccharomyces cerevisiae]	5.3
389	L15363	Human transfer RNA-Met (TRMEP1) pseudogene, complete gene	0.57	3228680	(AF070935) GABA receptor subunit [Musca domestica]	5.2
390	AE000525	Helicobacter pylori 26695 section 3 of 134 of the complete genome	0.57	1938478	(U97008) weak similarity to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	4.0
391	AF020189	Amblyomma americanum ecdysteroid receptor (AamEcR) mRNA, 3'UTR, region 1	0.57	2072224	(U94875) p40 [Borna disease virus]	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human UbA52 gene coding for ubiquitin-52 amino acid fusion protein				
392	X56997		0.57	2960113	(AL022121) hypothetical protein Rv3689	4.0
393	AL010260	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence	0.57	117233	CYTOCHROME P450 2C14 (CYPIIC14) phenobarbital-inducible, hepatic - rabbit P-450 [Oryctolagus cuniculus] >gi 358265 prt 1306317A cytochrome P450 [Oryctolagus cuniculus]	3.9
394	M99581	Xenopus laevis gamma-crystallin (gcry3) gene, complete cds.	0.57	141647	GASTRULA ZINC FINGER PROTEIN XLCGF44.2 >gi 85736 pir S06571 finger protein (clone XlcGF44-2) - African clawed frog (fragment)	3.0
395	M38384	Drosophila melanogaster seven in absentia mRNA, complete cds.	0.57	1707127	(U80454) T16A1.1 [Caenorhabditis elegans]	3.0
396	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.57	1173433	IRON(III)-TRANSPORT SYSTEM PERMEASE PROTEIN SFUB >gi 152861 (M33815) protein (sufB)	2.3
397	X12600	Klebsiella pneumoniae nifX, nifU, nifS, nifV and nifW genes	0.57	2909562	(AL021925) hypothetical protein Rv2256c	1.4
398	AB014526	Homo sapiens mRNA for KIAA0626 protein, complete cds	0.57	482390	insect-stage-specific protein - Trypanosoma cruzi >gi 162099 (M65021) insect stage-specific antigen	0.61
399	AF063587	Rhodococcus fascians strain NRRL-B-15096 hypothetical protein gene, complete cds	0.57	4104321	(AF034582) vesicle associated protein [Rattus norvegicus]	0.46
400	L11117	Guinea pig estrone sulfotransferase gene.	0.57	82584	alpha/beta-gliadin precursor (clone A212) - wheat	0.35

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
401	V00829	Mouse complete gene for a mouse kallikrein gene. Genes are mGK1 (complete gene) and mGK-2 of hormones, e.g., grow... > :: gb J00390 MUSKAL07 Mouse pseudo-kallikrein 2, exons 4 and 5, and kallikrein 1 gene, complete cds.	0.57	2500916	NUCLEAR HORMONE RECEPTOR NOR-2 receptor [Rattus norvegicus] >gi 1583604 prf 2121281A NOR-2 protein [Rattus norvegicus]	0.20
402	X53092	Chicken mRNA for beta-2 subunit of neuronal nicotinic acetylcholine receptor	0.57	1072256	(U40953) similar to matrin F/G (SP:Q00910) containing C4-type zinc-fingers [Caenorhabditis elegans] (Z81035) predicted using Genefinder; Similarity to dehydrogenases; cDNA EST EMBL:D65800 comes from this gene; cDNA EST EMBL:D76184 comes from this gene; cDNA EST EMBL:D69322 comes from this gene; cDNA EST EMBL:C08158 comes f...	0.031
403	L07939	Ovis ovis granulocyte colony stimulating factor	0.57	3874345	(AC003974) putative ubiquitin specific protease TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) >gi 107549 pir A35797 probable DNA-binding protein A20 - human >gi 177866 (M59465) A20	3e-07
404	U18061	Colletotrichum gloeosporioides CAP20 (cap20) gene, complete cds.	0.57	2914695	(AC003974) putative ubiquitin specific protease TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) >gi 107549 pir A35797 probable DNA-binding protein A20 - human >gi 177866 (M59465) A20	9e-08
405	Z73955	L.japonicus mRNA for small GTP-binding protein, RAB11G	0.57	112894	(M59465) A20	7e-08

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
406	X04335	Petunia grp-1 gene for glycine-rich protein	0.57	3876901	(Z77660) Similarity to Human enoyl-CoA hydratase (SW:ECHM_HUMAN); cDNA EST EMBL:T00611 comes from this gene; cDNA EST yk203d10.3 comes from this gene; cDNA EST yk203d10.5 comes from this gene; cDNA EST yk457h5.3 comes from t...	1e-27
407	U40718	Rattus norvegicus S-adenosylmethionine decarboxylase (AMDP2) pseudogene	0.56	<NONE>	<NONE>	<NONE>
408	M60318	S.cerevisiae SSD1 protein gene, complete cds. > :: gb AR013983 AR013983 Sequence 8 from patent US 5773245	0.56	<NONE>	<NONE>	<NONE>
409	X60057	Nicotiana tabacum blp4 mRNA for luminal binding protein (BiP)	0.56	<NONE>	<NONE>	<NONE>
410	AF085930	Homo sapiens full length insert cDNA clone YR55A09	0.56	<NONE>	<NONE>	<NONE>
411	AL010189	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence	0.56	<NONE>	<NONE>	<NONE>
412	X05402	Murine G-CSF gene for granulocyte colony stimulating factor precursor	0.56	<NONE>	<NONE>	<NONE>
413	U92280	Rattus norvegicus regulator of G-protein signalling 12 (RGS12) mRNA, complete cds	0.56	<NONE>	<NONE>	<NONE>
414	U85660	Human papillomavirus strain RTRX7 complete genome	0.56	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
415	X57626	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes	0.56	<NONE>	<NONE>	<NONE>
416	AB003363	Sus scrofa S100C gene, complete cds	0.56	<NONE>	<NONE>	<NONE>
417	L42291	Danio rerio DANA element, intron 4.	0.56	2650002	(AE001062) conserved hypothetical protein [Archaeoglobus fulgidus]	8.7
418	AF031826	Mus musculus leukocystatin gene, complete cds	0.56	462493	L-LACTATE DEHYDROGENASE (IMMUNOGENIC PROTEIN P36) >gi 479296 pir S33362 L-lactate dehydrogenase (EC 1.1.1.27) - Mycoplasma hyopneumoniae	6.7
419	U17068	Pennisetum glaucum Ac-like element, AcL2.	0.56	399449	ESCARGOT/SNAIL PROTEIN HOMOLOG	6.7
420	Z48042	H.sapiens mRNA encoding GPI-anchored protein p137	0.56	141232	HYPOTHETICAL 8.7 KD PROTEIN (READING FRAME D) >gi 76316 pir QQA7C hypothetical protein E-74	6.7
421	AF027657	Choristoneura fumiferana entomopoxvirus nucleotide triphosphate phosphohydrolase I (NPHI) gene, complete cds	0.56	464999	PUTATIVE ACETYLCHOLINE REGULATOR UNC-18 >gi 480359 pir S36747 acetylcholine regulator unc-18 - Caenorhabditis elegans >gi 247392 bbs 100294 putative acetylcholine regulator unc-18	5.1
422	AB011540	Homo sapiens mRNA for MEGF7, partial cds	0.56	1718033	URACIL-DNA GLYCOSYLASE (UDG) herpesvirus 2 >gi 695219 (U20824) uracil DNA glycosylase	5.1
423	X59941	X.maculatus NGF gene for nerve growth factor	0.56	1169081	COMMON PLANT REGULATORY FACTOR CPRF-1 >gi 515621 (X58575) light-inducible protein CPRF-1 [Petroselinum crispum] >gi 1498301 (U46217) CPRF1	3.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
424	M72711	Rat transcriptional repressor of myelin-specific genes (SCIP) mRNA, complete cds.	0.56	501027	(U01849) ORF2 [Trypanosoma brucei]	2.3
425	AL023850	Caenorhabditis elegans cosmid Y67D11A, complete sequence [Caenorhabditis elegans]	0.56	266771	CHORISMATE MUTASE (CM) / PREPHENATE DEHYDRATASE (PDT) (P-PROTEIN) >gi 281791 pir S26053 chorismate mutase (EC 5.4.99.5) P / prephenate dehydratase (EC 4.2.1.51) - Erwinia herbicola >gi 43344	2.3
426	U47862	Schistosoma mansoni gynecophoral canal protein mRNA, complete cds	0.56	2147138	ATP synthase chain 6 - Platymonas subcordiformis mitochondrion >gi 633582 (Z47797) ATP synthase subunit 6 [Platymonas subcordiformis]	2.3
427	V00574	Human germ line gene homologous to bladder carcinoma oncogene T24 (Gene code c-Ha-ras-1) with four exons.	0.56	1518672	(U60289) receptor protein tyrosine phosphatase psi [Homo sapiens]	1.7
428	Z71502	X.lacvis H1(0)-1 gene	0.56	1651674	(D90899) ferrichrome-iron receptor	1.3
429	M37278	R.norvegicus renin gene, exons 1-9.	0.56	2853019	(AF045141) putative serine proteinase [Scirpophaga incertulas]	1.0
430	D28878	Thermus thermophilus polA gene for thermostable DNA polymerase I, complete cds	0.56	3659692	(AF068748) sphingosine kinase [Mus musculus]	0.77
431	Z15027	H.sapiens HLA class III DNA	0.56	1304141	(D43758) fibrinogen A-alpha-chain	0.76
432	M14362	Human T-cell surface antigen CD2 (T11) mRNA, complete cds.	0.56	2462979	(Y11915) Tenascin-X [Bos taurus]	0.59
433	Z50801	Z.mays mRNA for chlorophyll a/b-binding protein CP29	0.56	109677	collagen alpha 1(I) chain - mouse >gi 50487	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
434	Z38114	<i>S.cerevisiae</i> chromosome XIII cosmid 9745	0.56	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (<i>Saccharomyces cerevisiae</i>)	0.35
435	AF052254	<i>Escherichia coli</i> DNA gyrase A (gyrA) gene, partial cds	0.56	2724126	(AF038535) synaptotagmin VII [<i>Homo sapiens</i>]	0.12
436	AF080649	<i>Tegula pulligo</i> 12S small subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence	0.56	3913223	CYCLIN-DEPENDENT KINASE INHIBITOR 1 p21/WAF1 [<i>Felis catus</i>]	0.11
437	AJ005690	<i>Danio rerio</i> mRNA for protein tyrosine kinase	0.56	2623830	(AF030962) unknown [<i>Schistosoma mansoni</i>]	7e-06
438	U31202	Human noggin (NOGGIN) gene, complete cds.	0.56	3875475	(Z78411) F02D8.3 [<i>Caenorhabditis elegans</i>]	1e-06
439	X51695	<i>Ovis sp.</i> trichohyalin mRNA, partial	0.56	3386622	(AC004665) unknown protein [<i>Arabidopsis thaliana</i>]	1e-10
440	U28938	<i>Rattus norvegicus</i> protein tyrosine phosphatase D30 mRNA, complete cds	0.56	3293547	(AF072709) putative oxidoreductase [<i>Streptomyces lividans</i>]	1e-14
441	AE001171	<i>Borrelia burgdorferi</i> (section 57 of 70) of the complete genome	0.56	2315521	(AF016452) similar to the beta transducin family	4e-16
442	AF036685	<i>Caenorhabditis elegans</i> cosmid C05B10	0.56	1519671	(U67951) contains similarity to ATP/GTP-binding site motif (PS:PS00017) [<i>Caenorhabditis elegans</i>]	6e-20
443	X01173	<i>Xenopus laevis</i> vitellogenin gene A1 5' flanking region	0.56	1118102	(U41558) K02B2.3 gene product [<i>Caenorhabditis elegans</i>]	2e-31
444	D10911	<i>Mus musculus</i> DNA for MS2 protein, complete cds	0.55	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Rice mRNA EN117,				
445	D30010	partial sequence	0.55	<NONE>	<NONE>	<NONE>
446	U51991	Escherichia coli phosphoprotein phosphatase	0.55	<NONE>	<NONE>	<NONE>
447	M18858	Mouse T cell receptor C-gamma-7.1 mRNA, 3' end.	0.55	<NONE>	<NONE>	<NONE>
448	U95218	Homo sapiens T cell-death associated protein gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
449	M14948	Human R-ras gene, exon 1.	0.55	<NONE>	<NONE>	<NONE>
450	AB002353	Human mRNA for KIAA0355 gene, complete cds	0.55	<NONE>	<NONE>	<NONE>
451	L81689	Homo sapiens (subclone 1_d6 from P1 H54) DNA sequence	0.55	<NONE>	<NONE>	<NONE>
452	M68955	Human myristoylated alanine-rich C-kinase substrate (MACS) gene, 5' end.	0.55	3322710	(AE001220) V-type ATPase, subunit B (atpB-1) [Treponema pallidum]	5.0
453	X62953	R.norvegicus mRNA (pJG116) with repetitive elements	0.55	1076802	extensin-like protein - maize >gi 600118 mays]	5.0
454	L34630	Synechocystis sp. mntABC transporter system: periplasmic-binding protein (mntC), complete cds; (mntA) gene, complete cds; membrane protein (mntB) gene, complete cds.	0.55	2117632	hydrogen dehydrogenase (EC 1.12.1.2) - Clostridium acetobutylicum >gi 557064 (U15277) hydrogenase I [Clostridium acetobutylicum]	5.0
455	U43521	Plasmodium berghei merozoite surface protein-1 gene, complete cds	0.55	127654	MYOGLOBIN	4.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
456	Z64937	H.sapiens CpG DNA, clone 17g7, reverse read cpg17g7.r1a.	0.55	417298	MFS18 PROTEIN PRECURSOR	3.8
457	U10914	Macaca mulatta clone irh83 T-cell receptor alpha chain mRNA, partial cds.	0.55	310406	(L09212) tat protein [Simian immunodeficiency virus] virus]	3.8
458	AF022838	Homo sapiens multidrug resistance protein	0.55	1585251	traB gene [Amycolatopsis methanolica]	2.8
459	M35603	Mouse Hox-3.1 gene and Hox-3.2-Hox-3.1 intergenic region.	0.55	818849	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]	2.0
460	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
461	AE001395	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence	0.55	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	1.7
462	U59736	Human transcription factor (NFATc.b) mRNA, complete cds	0.55	3327144	(AB014565) KIAA0665 protein [Homo sapiens]	0.096
463	U34860	Saccharomyces cerevisiae origin recognition complex large subunit (ORC1) gene, complete cds	0.55	140372	HYPOTHETICAL 86.0 KD PROTEIN IN GLK1-SRO9 INTERGENIC REGION >gi 83159 pir S19367 hypothetical protein YCL039w - yeast (Saccharomyces cerevisiae)	0.017
464	AF012341	Homo sapiens glutaryl-CoA dehydrogenase (GCDH) gene, exons 6, 7, 8, 9, and 10	0.55	1166611	(U46674) coded for by C. elegans cDNA yk27d9.5; coded for by C. elegans cDNA yk27d9.3; short region of weak homology to drosophila suppressor of sable protein	0.008

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		HIV-1 isolate Q98-				
465	AF004891	CxA from Kenya, envelope glycoprotein C2V3 region (env) gene, partial cds	0.54	<NONE>	<NONE>	<NONE>
466	Y10159	D.discoideum racGAP gene	0.54	<NONE>	<NONE>	<NONE>
467	AB001895	Homo sapiens mRNA for B120, complete cds	0.54	<NONE>	<NONE>	<NONE>
468	X12357	Bovine gene for aspartyl protease NM1 exons 3 and 4 > :: lcl[X12357 Bovine aspartyl protease NM1 gene, exons 3 and 4.	0.54	<NONE>	<NONE>	<NONE>
469	AE001151	Borrelia burgdorferi (section 37 of 70) of the complete genome	0.54	<NONE>	<NONE>	<NONE>
470	X92052	H.sapiens mRNA for T cell receptor alpha chain	0.54	<NONE>	<NONE>	<NONE>
471	U00938	Mus musculus ileal lipid-binding protein gene, complete cds	0.54	1009712	(U27698) calreticulin [Arabidopsis thaliana]	4.9
472	X68367	M.thermoformicum complete plasmid pFZ1 DNA	0.54	125272	CASEIN KINASE II, ALPHA CHAIN (CK II) >gi 419938 pir A43297 casein kinase II (EC 2.7.1.-) alpha chain - Theileria parva >gi 161871 (M92084) casein kinase II alpha subunit [Theileria parva]	4.7
473	Z61098	H.sapiens CpG DNA, clone 44c4, reverse read cpg44c4.rt1a.	0.54	4191274	(AJ131094) Xvent-1B protein [Xenopus laevis]	3.7
474	M63962	Human gastric H.K-ATPase catalytic subunit gene, complete cds.	0.54	3881648	(Z70757) similar to serine protease inhibitor [Caenorhabditis elegans]	3.7
475	X86019	H.sapiens mRNA for PRPL-2 protein	0.54	1648828	(D87963) ETF-related factor-1 (ETFR-1)	2.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
476	X89010	<i>S. glaucescens</i> genes strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides	0.54	3550345	(AF084524) cellular repressor of E1A-stimulated genes CREG [Mus musculus]	0.25
477	AB007836	Homo sapiens mRNA for Hic-5, partial cds	0.54	1097213	ORF 1 [Streptomyces lavendulae]	0.15
478	U32622	Comamonas testosteroni TsaR (tsaR), toluenesulfonate methyl-monooxygenase oxygenase component component (tsaB), toluenesulfonate zinc-independent alcohol dehydrogenase...	0.54	3875351	(Z96047) DY3.6 [Caenorhabditis elegans]	0.006
479	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
480	D61394	Arabidopsis thaliana gene for beta-VPE, complete cds	0.53	<NONE>	<NONE>	<NONE>
481	Z33072	M. capricolum DNA for CONTIG MC097	0.53	<NONE>	<NONE>	<NONE>
482	U45975	Human phosphatidylinositol (4,5)bisphosphate 5-phosphatase homolog mRNA, partial cds.	0.53	<NONE>	<NONE>	<NONE>
483	Z71324	S. cerevisiae chromosome XIV reading frame ORF YNL048w	0.53	2135586	M130 antigen (cytosolic variant 1) - human	2.1
484	L32090	Listeria monocytogenes secA gene, complete cds.	0.53	2291129	(AF016415) No definition line found [Caenorhabditis elegans]	0.70

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus mRNA				
485	D86423	for HGT keratin, partial cds	0.53	1235974	(X96713) collagen [Globodera pallida]	0.41
486	Y15969	Mus musculus V kappa 21-6 gene, partial	0.52	<NONE>	<NONE>	<NONE>
487	M27480	Mus musculus (clone 3F9) transcribed germline T cell receptor gamma chain (Tcr-g) mRNA, VJ4 C4 region.	0.52	3875542	(Z67990) Similarity to Rat amiloride-sensitive sodium channel beta-subunit	4.6
488	D87004	Human (lambda) DNA for immunoglobulin light chain	0.52	1766073	(U37272) winged helix protein CWH-1 [Gallus gallus]	3.5
489	Z99704	Human DNA sequence from cosmid E75B8 on chromosome 22, complete sequence [Homo sapiens]	0.51	<NONE>	<NONE>	<NONE>
490	U76523	Sambucus nigra lectin precursor mRNA, complete cds	0.51	<NONE>	<NONE>	<NONE>
491	U32795	Haemophilus influenzae Rd section 110 of 163 of the complete genome	0.50	<NONE>	<NONE>	<NONE>
492	M14602	Human myoglobin gene, exon 2.	0.49	478384	helicase homolog g10L protein - African swine fever virus >gi414091 (X72951) G10L 125 KDa protein	7.0
493	D87075	Human mRNA for KIAA0238 gene, partial cds	0.24	1938429	(U97002) similar to Schizosaccharomyces pombe 4-nitrophenylphosphatase (PNPPASE) (SP:Q00472, NID:g5004) [Caenorhabditis elegans]	2.5
494	U95102	Xenopus laevis mitotic phosphoprotein 90 mRNA, complete cds	0.23	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>N.crassa</i>				
495	J05254	mitochondrial small (19S) rRNA and Cys-tRNA.	0.23	192150	(L05670) clustrin [Mus musculus]	5.1
496	X16399	Gene for glutamate dehydrogenase (EC 1.4.1.4), put. bacterial origin	0.23	790933	(L07867) invariant surface glycoprotein [Trypanosoma brucei]	0.030
497	AE001251	Treponema pallidum section 67 of 87 of the complete genome	0.22	<NONE>	<NONE>	<NONE>
498	AF026919	Homo sapiens amyloid lambda light chain variable region mRNA, partial cds	0.21	<NONE>	<NONE>	<NONE>
499	Z27247	D.melanogaster mRNA for defensin	0.21	<NONE>	<NONE>	<NONE>
500	Y15608	Candida albicans UBI3 gene	0.21	<NONE>	<NONE>	<NONE>
501	V00598	Human beta-tubulin pseudogene.	0.21	<NONE>	<NONE>	<NONE>
502	X79426	A.thaliana microsatellite [repeated motif (gat)7]	0.21	<NONE>	<NONE>	<NONE>
503	X75772	A.caerulescens mitochondrial genes for cytochrome b and NADH dehydrogenase 5	0.21	139626	PROTEIN T1 PRECURSOR	7.8
504	AF028736	Serratia marcescens site specific recombinase	0.21	3645960	(AL031583) 1-evidence=predicted by content; 1-method=genefinder;084; 1-method_score=47.46; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=SWISS-PROT:P23792; 2-match_description=DISCONNECTED PROTEIN.; 2-mate...	4.6
505	X97545	S.cerevisiae OST5 gene	0.21	2275631	(AF014940) No definition line found [Caenorhabditis elegans]	2.7

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
506	M24543	Human prostate-specific antigen (PA) gene, complete cds.	0.21	1938527	(U97012) C04E6.2 gene product [Caenorhabditis elegans]	2.7
507	M62470	Mouse thrombospondin (THBS1) gene, complete cds.	0.21	548563	RNA REPLICASE POLYPROTEIN 2.7.7.48) - Erysimum latent virus >gi 3892232 (AF098523) replicase protein [Erysimum latent virus]	2.1
508	Y13544	Homo sapiens cosmid C1	0.21	1235710	(L40584) polyprotein [Infectious pancreatic necrosis virus]	2.0
509	M24193	Chicken MHC B complex protein (C12.3) mRNA, complete cds.	0.21	3600102	(AF090441) extracellular reelin [Gallus gallus]	0.52
510	X97161	H.sapiens TFE3 gene, exon 4,5 & 6	0.21	854065	(X83413) U88 [Human herpesvirus 6]	0.30
511	X67649	R.norvegicus DNA sequence for LFB1/HNF1 promoter	0.21	3913114	TRANSCRIPTION FACTOR COUP 2 COUP-TFII - chicken >gi 392817 (U00697) orphan receptor COUP-TFII [Gallus gallus]	0.004
512	U63807	Fugu rubripes growth hormone (GH) gene, complete cds	0.21	3510505	(AF030881) pol polyprotein [Fugu rubripes]	3e-04
513	Z95636	H.sapiens mRNA for laminin alpha 5 chain	0.21	400350	NAM7 PROTEIN (NONSENSE MEDIATED MRNA DECAY PROTEIN 1) (UP-FRAMESHIFT SUPPRESSOR 1) factor NAM7 - yeast (Saccharomyces cerevisiae) >gi 4023	1e-07
514	U91907	Mirounga leonina major histocompatibility complex class II (DQA) gene, partial cds	0.20	<NONE>	<NONE>	<NONE>
515	Z35758	Transmissible gastroenteritis virus TFI virion protein genes	0.20	<NONE>	<NONE>	<NONE>
516	X00334	Drosophila virilis simple DNA sequence (pDv-19)	0.20	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
517	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	0.20	<NONE>	<NONE>	<NONE>
518	D78515	Mus musculus rae28 gene, exon 1 and 5'flanking region	0.20	<NONE>	<NONE>	<NONE>
519	M62975	Drosophila melanogaster RNA polymerase II second largest subunit upstream (DmRP 140) gene, exons 1-4.	0.20	<NONE>	<NONE>	<NONE>
520	M27260	Chicken 78-kD glucose-regulated protein, complete cds.	0.20	<NONE>	<NONE>	<NONE>
521	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
522	AF076470	Rice tungro bacilliform virus Serdang strain, complete genome	0.20	<NONE>	<NONE>	<NONE>
523	U04636	Human cyclooxygenase-2 (hCox-2) gene, complete cds.	0.20	<NONE>	<NONE>	<NONE>
524	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.20	<NONE>	<NONE>	<NONE>
525	AF043514	Mus musculus phosphomannomutase (Pmm2) mRNA, complete cds	0.20	3025006	HYPOTHETICAL 15.5 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION >gi1787009 (AE000181) orf, hypothetical protein [Escherichia coli]	9.8

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
526	U23144	Xenopus laevis FTZ-F1-related nuclear orphan receptor variant (xFF1rAshort) mRNA, complete cds.	0.20	3184402	(AB014477) period protein [Chymomyza costata]	9.6
527	U14621	Paracentrotus lividus Pax-6 (suPax-6) mRNA, complete cds.	0.20	465894	PROBABLE MICROSOMAL SIGNAL PEPTIDASE 23 KD SUBUNIT (SPC22/23) >gi 630688 pir S44854 K12H4.4 protein - Caenorhabditis elegans >gi 289708 (L14331) homology with signal peptidase; coded for by C. elegans cDNAs GenBank: M79661, M79662 and M79663; putative	7.7
528	AF030511	Actinobacillus pleuropneumoniae MRP ATPase homolog (mrp) gene, partial cds; ApxIVA var3 (apxIVA) gene, complete cds; and beta-galactosidase (lacZ) gene, partial cds	0.20	1175966	HYPOTHETICAL 45.3 KD PROTEIN IN THIS 5'REGION >gi 1084720 pir S56193 probable membrane protein YFL062w - yeast (Saccharomyces cerevisiae)	7.2
529	AF070581	Homo sapiens clone 24540 mRNA sequence	0.20	542394	glyoxal oxidase (EC 1.2.3.-) precursor - basidiomycete (Phanerochaete chrysosporium) >gi 1050302	5.8
530	X75437	T.maritima pgK gene for 3-phosphoglycerate kinase	0.20	825648	(Z34531) coproporphyrinogen oxidase [Homo sapiens]	5.8
531	U32686	Haemophilus influenzae Rd section 1 of 163 of the complete genome	0.20	3309593	(AF072878) ciliary outer arm dynein beta heavy chain	5.6
532	Z28081	S.cerevisiae chromosome XI reading frame ORF YKL081w	0.20	2507201	CARBON CATABOLITE DEREPRESSING PROTEIN KINASE >gi 1469803 (L78129) serine/threonine kinase [Candida albicans]	5.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Hordeum vulgare				
533	AF022725	limit dextrinase (HvLD99) gene, complete cds	0.20	3139154	(AF064077) adrenocorticotrophic hormone receptor [Sus scrofa]	4.3
534	AL021726	Drosophila melanogaster cosmid 171E4	0.20	3885334	(AC005623) putative argonaute protein [Arabidopsis thaliana]	2.6
535	AB012106	Brassica rapa mRNA for SRK45, complete cds	0.20	4008334	(Z92824) B0413.4 [Caenorhabditis elegans]	1.5
536	Z46606	H.sapiens HLTF gene for helicase-like transcription factor	0.20	132946	60S RIBOSOMAL PROTEIN L30B (RP29) cytosolic - yeast (Saccharomyces cerevisiae) >gi 171821 not determined [Saccharomyces cerevisiae] >gi 1045254 cerevisiae] >gi 1323250 gnl PID e243708 (Z72933) ORF YGR148c [Saccharomyces cerevisiae]	1.5
537	X87193	H.sapiens mRNA for 2.19 gene	0.20	139820	DNA-REPAIR PROTEIN XRCC1	1.5
538	L77965	Clostridium perfringens C beta 2 toxin gene, complete cds	0.20	1175950	HYPOTHETICAL 33.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION >gi 1084703 pir S56211 probable membrane protein YFL044c - yeast (Saccharomyces cerevisiae) >gi 836711 gnl PID d1009835 (D50617) YFL044C	1.4
539	M15938	Chicken neural cell-adhesion molecule (NCAM) gene, exon 18.	0.20	2133082	regulatory protein MSR1 - yeast	1.1
540	AJ003220	Solanum tuberosum mRNA for extensin-like protein, partial	0.20	2496932	HYPOTHETICAL 55.9 KD PROTEIN C56G2.1 IN CHROMOSOME III >gi 726413 (U23177) C56G2.1 gene product [Caenorhabditis elegans]	1.1
541	X98108	A.thaliana psbP gene	0.20	119227	EPIDERMAL GROWTH FACTOR PRECURSOR precursor - mouse >gi 309210 (J00380) prepro-egf [Mus musculus]	0.49

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
542	AB011179	Homo sapiens mRNA for KIAA0607 protein, partial cds	0.20	2143753	gene VGF protein - rat >gi 205690 (M60525) nerve growth factor inducible protein [Rattus norvegicus] >gi 205701 (M60522) nerve growth factor-inducible protein [Rattus norvegicus] >gi 207651	0.39
543	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.20	629557	RNA-binding protein rnpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.38
544	AB008374	Oncorhynchus mykiss mRNA for alpha 3 type I collagen, partial cds	0.20	1082610	muf1 protein - human >gi 762953 (X86018) muf1 [Homo sapiens]	0.37
545	U09809	Limulus polyphemus arginine kinase mRNA, complete cds.	0.20	3882016	(AJ012650) CP [Papaya ringspot virus]	0.37
546	AB020671	Homo sapiens mRNA for KIAA0864 protein, partial cds	0.20	2674350	(U93121) M-phase phosphoprotein-1 [Homo sapiens]	0.18
547	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.043
548	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.20	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.042

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
549	S82819	Cdk5 α -cyclin-dependent kinase 5 regulatory subunit p35 [mice, brain, 129/SvJ, C57BL/6, Genomic/mRNA, 5528 nt]	0.20	3413870	(AB007923) KIAA0454 protein (Homo sapiens)	0.020
550	D31792	Streptomyces griseus DNA for serine/threonine protein kinases, complete cds	0.20	861405	(U29154) T07F12.2 gene product [Caenorhabditis elegans]	0.019
551	U97499	Homo sapiens butyrophilin (BT3.2) gene, exons 5-10, and complete cds	0.20	2773341	(AF040954) putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]	0.008
552	U31463	Rattus norvegicus nonmuscle myosin heavy chain-A mRNA, complete cds.	0.20	3880111	(Z81130) predicted using Genefinder	0.002
553	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of lysis gene 13	0.20	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	4e-04
554	X57310	Nocardia lactamdurans pcbAB and pcbC genes for alpha-aminoadipyl-L-cysteinyl-D-valine synthetase and isopenicillin N synthase	0.20	1723511	PUTATIVE ENDONUCLEASE C1F12.06C yeast (Schizosaccharomyces pombe) >gi 1217980 (Z69944) unknown [Schizosaccharomyces pombe]	4e-09
555	X62386	S.epidermidis genes epiY, epiY, epiA, epiB, epiC, epiD, epiQ, epiP	0.20	3874927	(Z73424) C44B9.1 [Caenorhabditis elegans]	3e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
556	X59000	Epizootic haemorrhagic disease virus gene segment 6 for NS1	0.20	3879755	(Z80220) similar to nucleotide binding protein; cDNA EST EMBL:M75897 comes from this gene; cDNA EST EMBL:M89054 comes from this gene; cDNA EST EMBL:D26713 comes from this gene; cDNA EST EMBL:D26718 comes from this gene; cDNA...	8e-16
557	M98776	Human keratin 1 gene, complete cds	0.20	1086900	(U41278) contains similarity to G beta repeats	2e-30
558	AF011446	Mus musculus granzyme K gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
559	AF074708	Macaca mulatta clone MMU1.5 FRG1-like pseudogene, exons 7 and 8, partial sequence	0.19	<NONE>	<NONE>	<NONE>
560	X13287	Medicago sativa nodulin-25 gene	0.19	<NONE>	<NONE>	<NONE>
561	Z49509	S.cerevisiae chromosome X reading frame ORF YJR009c	0.19	<NONE>	<NONE>	<NONE>
562	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.19	<NONE>	<NONE>	<NONE>
563	D29644	Streptococcus salivarius DNA for dextranase	0.19	<NONE>	<NONE>	<NONE>
564	AE001461	Helicobacter pylori, strain J99 section 22 of 132 of the complete genome	0.19	<NONE>	<NONE>	<NONE>
565	L38559	Homo sapiens galactocerebrosidase (GALC) gene, exon 17.	0.19	<NONE>	<NONE>	<NONE>
566	Z82628	R.prowazekii genomic DNA fragment (clone A-405F)	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
567	U25641	Tetrahymena thermophila telomerase component p80 mRNA, complete cds	0.19	<NONE>	<NONE>	<NONE>
568	AB002343	Human mRNA for KIAA0345 gene, complete cds	0.19	<NONE>	<NONE>	<NONE>
569	D10064	Erwinia carotovora gene for pectate lyase III, complete cds	0.19	<NONE>	<NONE>	<NONE>
570	U31734	Homo sapiens clone MF118 A4A10 hypoxanthine phosphoribosyltransferase (hprt) 130 kb deletion mutant mRNA, partial cds, contains human Alu element	0.19	<NONE>	<NONE>	<NONE>
571	AE001386	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence	0.19	<NONE>	<NONE>	<NONE>
572	M95623	Homo sapiens hydroxymethylbilane synthase gene, complete cds.	0.19	<NONE>	<NONE>	<NONE>
573	S67478	(GC*IS)=vitamin D-binding protein/group specific component [human, peripheral blood leukocytes, Genomic, 794 nt, segment 4 of 9]	0.19	<NONE>	<NONE>	<NONE>
574	X99075	H.sapiens NRGN gene, exon 1	0.19	<NONE>	<NONE>	<NONE>
575	AF044775	Homo sapiens breakpoint cluster region BCRder14 sequence	0.19	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human mRNA for KIAA0335 gene, complete cds				
576	AB002333		0.19	<NONE>	<NONE>	<NONE>
577	U53566	Macaca mulatta pit-1/GHF-1 transcription factor mRNA, complete cds	0.19	1078068	probable membrane protein YLR311c - yeast	9.2
578	U73664	Human t(11;14)(q13;q32) breakpoint junction sequence	0.19	116734	COAT PROTEIN (CAPSID PROTEIN) virus >gi58901 (X62133) CyMV coat protein gene product	8.8
579	AF004054	Heterophyllaea pustulata rps16 gene, chloroplast gene, partial intron sequence	0.19	1928991	(U92815) heat shock protein 70 precursor [Citrullus lanatus]	8.7
580	Z27081	Caenorhabditis elegans cosmid M01A8, complete sequence [Caenorhabditis elegans]	0.19	2496247	HYPOTHETICAL ATP-BINDING PROTEIN MJ0625 >gi2128413 pir A64378 hypothetical protein MJ0625 - Methanococcus jannaschii >gi1591336 (U67510) M. jannaschii predicted coding region MJ0625	8.6
581	Z74145	S.cerevisiae chromosome IV reading frame ORF YDL097c	0.19	1174425	TYROSINE-PROTEIN KINASE SPK-1	6.7
582	D38547	Small round structured virus genomic RNA, 3'terminal sequence containing ORF2 and ORF3	0.19	971318	(Z48053) putative protein [Bovine herpesvirus 1]	5.1

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
583	D88000	Ralstonia eutropha DNA 16S ribosomal RNA > :: dbj D88002 D88002 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj D88003 D88003 Ralstonia eutropha DNA for 16S ribosomal RNA > :: dbj D88004 D88004 Ralstonia eutropha DNA for 16S ribosomal RNA	0.19	3800952	(AF100657) No definition line found [Caenorhabditis elegans]	5.1
584	U67462	Methanococcus jannaschii section 4 of 150 of the complete genome	0.19	3183617	(AJ005586) MYB-related transcription factor [Antirrhinum majus]	4.0
585	L23906	Gallus domesticus microsatellite DNA marker.	0.19	1947094	(U93074) voltage-gated sodium channel homolog BdNa1	3.9
586	AE001462	Helicobacter pylori, strain J99 section 23 of 132 of the complete genome	0.19	1730177	GLUCOSE-6-PHOSPHATE ISOMERASE (GPI) ISOMERASE) (PHI) >gi 2118333 pir 148073 glucose phosphate isomerase - Chinese hamster >gi 987046 griseus] (Z82256) cDNA EST yk251g7.3 comes from this gene; cDNA EST yk251g7.5 comes from this gene; cDNA EST EMBL:D68223 comes from this gene; cDNA EST EMBL:C12737 comes from this gene; cDNA EST yk389c8.5 comes from this gene; cDNA E...	3.9
587	M19460	P.putida catBC operon encoding cis,cis-muconate lactonizing enzyme I and muconolactone isomerase genes, complete cds.	0.19	3873843		3.9
588	U22349	Tetrahymena australis telomerase RNA gene, complete sequence	0.19	4105782	(AF049922) PGP169-12 [Petunia x hybrida]	3.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
589	L27745	Homo sapiens voltage operated calcium channel, alpha-1 subunit mRNA, complete cds.	0.19	3763926	(AC004450) unknown protein [Arabidopsis thaliana]	3.0
590	AF049588	Canis familiaris synapsin I gene, partial cds	0.19	4104931	(AF042196) auxin response factor 8 [Arabidopsis thaliana]	3.0
591	X06627	Staphylococcus aureus plasmid pS194 sequence	0.19	137927	PRE-NECK APPENDAGE PROTEIN (LATE PROTEIN GP12) >gi 75856 pir WMBP22 gene 12 protein - phage phi-29 >gi 215330 (M14782) pre-neck appendage protein [Bacteriophage phi-29] >gi 225367 prf 1301270G gene 12 [Bacteriophage phi-29]	2.3
592	X61597	M.musculus gene for kallikrein-binding protein	0.19	2982874	(AE000675) cobalamin synthesis related protein CobW	1.7
593	AF016242	Dictyostelium discoideum protein synthesis elongation factor 1-alpha (tef2) gene, partial cds	0.19	133659	PUTATIVE RNA-DIRECTED RNA POLYMERASE	1.4
594	AF004447	Venezuelan equine encephalitis virus strain 1327 polypeptide gene, partial cds >:: gb AF004460 AF004460 Venezuelan equine encephalitis virus strain 1385 polypeptide gene, partial cds	0.19	4096173	(U25968) early embryogenesis protein [Oryza sativa]	1.3
595	J04821	Human elastin (ELN) gene, exon 1, clones HELC-5 and HELC-6.	0.19	1170523	INHIBIN BETA B CHAIN PRECURSOR inhibin precursor - bovine >gi 563753 (U16241) betaB inhibin/activin precursor [Bos taurus]	1.3
596	AF059650	Homo sapiens histone deacetylase 3 (HDAC3) gene, complete cds	0.19	3024881	PROBABLE TRANSPORT PROTEIN CY21C12.11 >gi 2078066 gnl PID e315171 (Z95210) betP	0.83

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
597	M69053	D.melanogaster calcium-activated K+ channel subunit	0.19	1707984	FERREDOXIN-DEPENDENT GLUTAMATE SYNTHASE I (FD-GOGAT) >gi 2126524 pir S60228 glutamate synthase (ferredoxin) (EC 1.4.7.1) gltB - Synechocystis sp. (PCC 6803) >gi 515938 (X80485) glutamate synthase	0.80
598	AF076279	Dictyostelium fimbriasis plasmid Dfp1, complete plasmid sequence	0.19	453986	(U00008) yejA [Escherichia coli]	0.79
599	D28873	Mouse MCNP gene for C-type natriuretic peptide, complete cds (exon1, exon2)	0.19	2650444	(AE001092) acetyl-CoA synthetase (acs-1) [Archaeoglobus fulgidus]	0.63
600	U06071	Oxytricha nova macronuclear actin II gene, complete cds.	0.19	1584024	complement control protein [Botryllus schlosseri]	0.48
601	L54057	Homo sapiens CLP mRNA, partial cds.	0.19	3036883	(AL022374) putative ABC transporter	0.46
602	X89806	P.lividius cDNA for COLL2alpha gene	0.19	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	0.41
603	AE001104	Archaeoglobus fulgidus section 3 of 172 of the complete genome	0.19	2315192	(Y11739) transcription factor [Homo sapiens]	0.35
604	U54501	Rattus norvegicus microsatellite sequence D0Mco22	0.19	228951	D-MeAsp receptor:ISOTYPE=epsilon3 [Mus musculus]	0.32
605	X74468	Human papillomavirus type 15 genomic DNA	0.19	3695390	(AF096371) contains similarity to Rattus norvegicus cyclin G-associated kinase (SW:P97874) [Arabidopsis thaliana]	0.28
606	U20285	Human Gps1 (GPS1) mRNA, complete cds	0.19	2582659	(AJ002527) glucitol-6-phosphate dehydrogenase [Clostridium beijerinckii]	0.27
607	D49408	Human gene for interleukin 3 receptor alpha subunit, exon 10	0.19	2522368	(AF008596) alpha1,3-fucosyltransferase [Helicobacter pylori]	0.16

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
608	AF041141	Homo sapiens pituitary specific homeodomain protein (PROP1) gene, exon 3 and complete cds	0.19	37403	(X03541) trk gene product (aa 1-641) [Homo sapiens]	0.091
609	L12531	Discopyge ommata Ca2+ channel alpha 1 subunit gene sequence.	0.19	3618274	(AJ223219) hypothetical protein	0.069
610	AF052445	Yellow fever virus clone HONG9 polyprotein gene, complete cds	0.19	1932822	(U15928) KH-domain putative RNA binding protein	0.001
611	Z36946	B.anthraxis sap gene encoding S-layer protein	0.19	173241	(L06487) ZIP1 protein [Saccharomyces cerevisiae]	2e-04
612	AF087984	Homo sapiens full length insert cDNA clone YW29A12	0.19	3786014	(AC005499) hypothetical protein [Arabidopsis thaliana]	1e-06
613	AE001010	Archaeoglobus fulgidus section 97 of 172 of the complete genome	0.19	3135493	(AF060248) unknown [Arabidopsis thaliana]	7e-08
614	L08965	Trichosporon cutaneum carbamoyl phosphate synthetase large subunit (argA) gene, partial cds.	0.19	1086901	(U41278) F33G12.3 gene product [Caenorhabditis elegans]	2e-08
615	M91466	Rattus norvegicus A2b-adenosine receptor mRNA, complete cds.	0.19	2984320	(AE000773) acetoin utilization protein [Aquifex acolicus]	6e-09
616	X95971	S.lividans groEL2 gene	0.19	3925277	(AL032643) similar to Uncharacterized protein family UPF0034, Double-stranded RNA binding motif; cDNA EST yk489b3.5 comes from this gene; cDNA EST yk439g7.5 comes from this gene [Caenorhabditis elegans]	7e-10
617	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	3e-14

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
618	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete cds.	0.19	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	9e-15
619	Z68327	Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.	0.19	3875774	EMBL:D32434 comes from this gene; cDNA EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ... >gi 3878710 gnl PID e1348373 EST EMBL:D33710 comes from this gene; cDNA EST EMBL:D34467 comes from this gene; cDNA EST EMBL:D35005 comes from this gene; cDNA EST EMBL:D37535 comes from this gene; ...	6e-15
620	U66525	Dictyostelium discoideum ORFveg114 mRNA, complete cds	0.19	3540281	(AF056116) All-1 related protein [Fugu rubripes]	2e-17
621	U25830	Newcastle disease virus isolate Herts/33 matrix protein mRNA, complete cds	0.19	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-18
622	U89407	Mus musculus strain BALB/c delta-aminolevulinic acid dehydratase (Lv) mRNA, partial cds	0.19	1825764	(U88314) C46H11.11 gene product [Caenorhabditis elegans]	3e-25
623	AF095598	Bison bison athabasca microsatellite BBJ 2	0.18	<NONE>	<NONE>	<NONE>
624	AF064260	Strongylocentrotus purpuratus SRC8 mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>

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SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
625	U69533	Arabidopsis thaliana AtKAP alpha mRNA, complete cds	0.18	<NONE>	<NONE>	<NONE>
626	D89041	Bovine DNA for prostaglandin F2alpha receptor, partial cds	0.18	<NONE>	<NONE>	<NONE>
627	M24571	Dictyostelium discoideum tRNA-Glu-GAA gene, clone yGluGAA7.	0.18	<NONE>	<NONE>	<NONE>
628	X59772	D.melanogaster ovo gene required for female germ line development	0.18	<NONE>	<NONE>	<NONE>
629	AL010209	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-104, complete sequence	0.18	<NONE>	<NONE>	<NONE>
630	U67575	Methanococcus jannaschii section 117 of 150 of the complete genome	0.18	111839	inositol 1,4,5-triphosphate receptor 2 - rat	8.5
631	U28730	Caenorhabditis elegans cosmid K10B2	0.18	1787604	(AE000232) orf, hypothetical protein [Escherichia coli]	8.3
632	X99798	L.lactis pepF1 & pepF2 genes	0.18	3406624	(AF079110) glycosomal malate dehydrogenase [Trypanosoma brucei]	8.1
633	AF025306	Danio rerio band 4.1-like protein 4 (nbl4) mRNA, complete cds	0.18	465445	PROBABLE NUCLEAR ANTIGEN herpesvirus 1 (strain Kaplan) >gi 334072 (M34651) ORF-3 protein [Pseudorabies virus]	7.9
634	AF059251	Mus musculus lipoxxygenase (alox) mRNA, complete cds	0.18	1655667	(Z81368) hypothetical protein Rv2393	6.6
635	Z22605	G.domesticus CTCF protein mRNA.	0.18	481864	3-methyl-2-oxobutanoate dehydrogenase	6.6
636	AB011086	Homo sapiens mRNA for KIAA0514 protein, complete cds	0.18	3874158	(Z81464) predicted using Genefinder	6.4

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
637	Z78536	Caenorhabditis elegans cosmid C07A4, complete sequence [Caenorhabditis elegans]	0.18	3702121	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]	6.4
638	U67530	Methanococcus jannaschii section 72 of 150 of the complete genome	0.18	3877946	(Z81094) Weak similarity to 65 KDA heat shock protein (TR:G602231); cDNA EST EMBL:D71705 comes from this gene; cDNA EST EMBL:D74382 comes from this gene [Caenorhabditis elegans] (Z69634) cDNA EST EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.3
639	M63781	Influenza A/Duck/England/1/62 (H4N6) nucleoprotein mRNA, complete cds.	0.18	3873663	EMBL:D71510 comes from this gene; cDNA EST EMBL:C08449 comes from this gene; cDNA EST yk266b12.3 comes from this gene; cDNA EST yk266b12.5 comes from this gene; cDNA EST yk461h7.3 comes from this gene; cDNA...	6.2
640	M73781	Oryctolagus cuniculus integrin beta-8 subunit mRNA, complete cds. > :: gb I44828 I44828 Sequence 3 from patent US 5635601	0.18	1362129	major allergen OLE17 - common olive	5.8
641	X67219	D.melanogaster Rop gene	0.18	3449286	(AB011527) MEGF1 [Rattus norvegicus]	4.8
642	AF106941	Homo sapiens beta-arrestin 2 mRNA, complete cds	0.18	548353	[PROTEIN-PII] URIDYLTRANSFERASE vinelandii >gi 39257 (X59610) uridylyl transferase	3.7
643	AF052602	Danio rerio huntingtin (HD) mRNA, complete cds	0.18	241058	potential IGF binding protein [chickens, Peptide Partial, 77 aa, segment 2 of 3]	3.6

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
644	AB020709	Homo sapiens mRNA for KIAA0902 protein, complete cds	0.18	3875570	(Z68314) predicted using Genefinder; cDNA EST EMBL:M75775 comes from this gene; cDNA EST EMBL:M89255 comes from this gene; cDNA EST EMBL:M89127 comes from this gene; cDNA EST EMBL:T00141 comes from this gene; cDNA EST EMBL:T...	2.1
645	AF096883	HIV-1 isolate patient 3 country USA pol polyprotein (pol) gene, partial cds	0.18	3250696	(AL024486) putative protein	1.7
646	L39928	Pyrococcus furiosus (clone pB-PmL41) luciferase mRNA, complete cds	0.18	2914702	(AC003974) unknown protein [Arabidopsis thaliana]	0.73
647	M17082	Human carcinoembryonic nonspecific crossreacting antigen (CEA; NCA) gene, exons 1 and 2.	0.18	1351833	REGULATORY PROTEIN ABAA	0.72
648	X75318	H.sapiens ITIH1 gene (exon 22) and ITIH3 gene	0.18	629557	RNA-binding protein mpD - Arabidopsis thaliana (fragment) >gi 510240 (X61108) RNA binding protein [Arabidopsis thaliana]	0.41
649	AF011908	Mus musculus apoptosis associated tyrosine kinase (AATYK) mRNA, complete cds	0.18	330442	(K03332) nuclear antigen 2 [Epstein-Barr virus]	5e-04
650	U04004	Simian immunodeficiency virus SIVagmVER-2 envelope protein gene, partial cds.	0.18	135102	ASPARTYL-TRNA SYNTHETASE aspartate--tRNA ligase (EC 6.1.1.12) - Escherichia coli coli >gi 1736513 gnl PID d1016401 (D90829) Aspartate--tRNA ligase (EC 6.1.1.12) [Escherichia coli]	6e-11
651	U88155	Xenopus laevis RanGTPase activating protein	0.18	995714	(X91258) pid:c198503 [Saccharomyces cerevisiae]	2e-13

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
652	Z18921	B.oleracea gene for S-receptor kinase-like protein	0.18	3875535	(Z66511) similar to ribokinase; cDNA EST EMBL:D69553 comes from this gene; cDNA EST EMBL:D65938 comes from this gene; cDNA EST yk280h9.3 comes from this gene; cDNA EST yk280h9.5 comes from this gene; cDNA EST yk223d11.3 come...	1e-19
653	M60650	S.cerevisiae STA2 gene, complete cds.	0.16	<NONE>	<NONE>	<NONE>
654	U80912	Eucalyptus globulus NADP-isocitrate dehydrogenase (EgICDH) mRNA, complete cds	0.16	3766172	(AF057298) ornithine decarboxylase antizyme 2 [Mus musculus]	4.2
655	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.16	76749	hypothetical protein 4 - fowl adenovirus 1	4.0
656	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.16	3044086	(AF055904) unknown [Myxococcus xanthus]	0.60
657	AF030231	Glycine max sucrose synthase (SS) mRNA, complete cds	0.078	<NONE>	<NONE>	<NONE>
658	M19183	Woodchuck hepatitis virus (WHV), complete genome, clone WHV 59.	0.072	1076190	cell wall glycoprotein, 75K, precursor - diatom (Cylindrotheca fusiformis) >gil515363 (X80394) P75K gene product [Cylindrotheca fusiformis]	6.3
659	U31557	Ovine adenovirus IVa2 protein gene, DNA polymerase gene, terminal protein gene and 52.55 kDa protein gene, partial cds	0.072	3511143	(AF061244) unknown [Agrocybe aegerita]	6.2

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
660	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.070	<NONE>	<NONE>	<NONE>
661	M33874	X.laevis Xotch protein mRNA, complete cds.	0.070	1654096	(Y09076) RAD3 [Schizosaccharomyces pombe]	0.23
662	AB012725	Mus musculus ZAN75 mRNA for zinc finger protein, complete cds	0.069	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	2.0
663	AL021491	Caenorhabditis elegans cosmid Y44A6B, complete sequence [Caenorhabditis elegans]	0.068	<NONE>	<NONE>	<NONE>
664	Z60318	H.sapiens CpG DNA, clone 1e1, reverse read cpg1e1.1a .	0.068	1280134	(U55376) F16H11.2 gene product [Caenorhabditis elegans]	2.6
665	Z35973	S.cerevisiae chromosome II reading frame ORF YBR104w	0.068	2493000	PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR EMBL:Z14816 comes from this gene; cDNA EST EMBL:Z14946 comes from this gene; cDNA EST EMBL:D69746 comes from this gene; cDNA EST yk219b6.3 comes from this gene; cDNA ES...	0.68
666	Z86111	Streptomyces lividans rpsP, trmD, rplS, sipW, sipX, sipY, sipZ, mutT genes and 4 open reading frames	0.068	1235974	(X96713) collagen [Globodera pallida]	4e-04
667	M72980	Anthonomus grandis vitellogenin gene (VTG), complete cds.	0.068	3242750	(AC005164) match to ESTs AA731149 (NID:g2140138), AA731908 (NID:g2752719), AA287837 (NID:g1933519), AA262811 (NID:g1898382), and AA825820 (NID:g2899132)	1e-59

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
668	M34161	Rat tachykinin (PPT) gene, exons 5 and 6.	0.067	<NONE>	<NONE>	<NONE>
669	L03811	Aspergillus niger zinc finger protein (creA) gene, complete cds.	0.067	<NONE>	<NONE>	<NONE>
670	M64983	Human fibrinogen beta chain gene, complete mRNA. >gb 147706 147706 Sequence 3 from patent US 5639940	0.067	<NONE>	<NONE>	<NONE>
671	AF014051	Nicotiana tabacum Mg chelatase subunit (ChlH) mRNA, partial cds	0.067	<NONE>	<NONE>	<NONE>
672	Y07540	H.sapiens sil gene	0.067	92331	glycoprotein GP330, renal - rat (fragments)	7.5
673	AJ000347	Rattus norvegicus mRNA for 3'(2'),5'-bisphosphate nucleotidase	0.067	129238	25 KD OOKINETE SURFACE ANTIGEN PRECURSOR (PRS25) >gi 320962 pir A44966 25k ookinete surface antigen precursor - Plasmodium reichenowi reichenowi]	7.4
674	L19979	Squid sodium channel mRNA, complete cds.	0.067	2128473	hypothetical protein MJ0750 - Methanococcus jannaschii >gi 1592304 (U67521) ferredoxin-type protein	1.5
675	X08050	Yeast tRNA-Glu(3) gene and flanking regions	0.067	1334398	(X15081) MURF2 protein (AA 1-348)	0.65
676	X17115	Human mRNA for IgM heavy chain complete sequence	0.067	1731331	HYPOTHETICAL 51.6 KD PROTEIN CY49.14C >gi 1370241 gnl PID e247089 (Z73966) hypothetical protein Rv2075c [Mycobacterium tuberculosis]	0.51
677	AF032871	Homo sapiens uncoupling protein 3 (UCP3) gene, exon 1 and partial exon 2	0.067	112900	ALPHA-2C-1 ADRENERGIC RECEPTOR human >gi 178194 (J03853) kidney alpha-2-adrenergic receptor [Homo sapiens] >gi 1628638 (U72648) alpha2-C4-adrenergic receptor [Homo sapiens]	0.50

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
					DYNAMIN 3 (DYNAMIN, TESTICULAR) rat	
678	X05319	Mouse class II MHC E-beta 2 (d) gene exon 3	0.067	585074	>gi 391872 gnl PID d1003668 (D14076) testicular dynamin [Rattus norvegicus]	3e-04
679	AB006362	Candida albicans CaSLN1 gene, complete cds	0.067	3417296	(AC003007) Unknown gene product (partial) [Homo sapiens]	9e-56
680	AF021236	African horse sickness virus capsid VP3 (L3) mRNA, complete cds	0.066	<NONE>	<NONE>	<NONE>
681	AE001507	Helicobacter pylori, strain J99 section 68 of 132 of the complete genome	0.066	<NONE>	<NONE>	<NONE>
682	AF039717	Caenorhabditis elegans cosmid R13H8	0.066	<NONE>	<NONE>	<NONE>
683	AF029027	Syncerus caffer isolate Queen Elizabeth Mweya 14 mitochondrial DNA control region	0.066	<NONE>	<NONE>	<NONE>
684	AF087967	Homo sapiens full length insert cDNA clone YU51G05	0.066	2982476	(X97203) C1 protein [Beet curly top virus]	9.5
685	J02037	Baboon endogenous virus proviral long terminal repeat DNA.	0.066	972767	(L37868) POU-domain transcription factor [Homo sapiens]	7.3
686	AF000141	Lycopersicon esculentum class I knotted-like homeodomain protein (LeT6) mRNA, complete cds	0.066	3157926	(AC002131) Strong similarity to extensin-like protein gb Z34465 from Zea mays. [Arabidopsis thaliana]	5.6
687	AB001746	Bensingtonia sp. OK255 gene for 18S rRNA > :: dbj AB001747 AB001747 Bensingtonia sp. OK259 gene for 18S rRNA	0.066	3859889	(AF070064) cap 'n' collar isoform C [Drosophila melanogaster]	0.38

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Helicobacter pylori</i> , strain J99 section 22 of 132 of the complete genome	0.065	<NONE>	<NONE>	<NONE>
688	AE001461					
689	M30821	Chicken erythroid transport proteins c1 and c2	0.065	<NONE>	<NONE>	<NONE>
690	AB009802	Homo sapiens gene for osteonidogen, intron 3	0.065	<NONE>	<NONE>	<NONE>
691	AF086062	Homo sapiens full length insert cDNA clone YZ06B11	0.065	<NONE>	<NONE>	<NONE>
692	AB002369	Human mRNA for KIAA0371 gene, complete cds	0.065	2500884	SIGNAL SEQUENCE BINDING PROTEIN binding protein [<i>Synechococcus</i> sp.]	5.5
693	AF086864	Cyclopodia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence > :: gb AF086866 AF086866 Penicillidia sp. large subunit ribosomal RNA gene, mitochondrial gene for mitochondrial RNAs, partial sequence	0.065	3721684	(AB012957) probable glycosyl transferase [<i>Vibrio cholerae</i>]	5.5
694	L44593	Bacteriophage BK5-T ORF410, 3' end pf cds, 20 ORFs, repressor protein, and Cro repressor protein genes, complete cds, ORF70' gene, 5' end of cds.	0.065	1172067	PEPTIDASE T (AMINOTRIPEPTIDASE) [influenzae Rd]	3.2
695	U80079	<i>Ciona intestinalis</i> MyoD-family protein (CiMDFa) mRNA, complete cds	0.065	4218110	(AL035353) contains EST gb:F15281	2.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
696	AB020718	Homo sapiens mRNA for KIAA0911 protein, complete cds	0.065	1722734	MINOR CAPSID PROTEIN L2 >gi 1020192 type 23]	1.9
697	AF082137	Zea mays copia-like retrotransposon Stl-14 leader region, partial sequence	0.065	1877501	(U89278) polyhomeotic 2 homolog [Homo sapiens]	1.1
698	X64053	R.norvegicus ZnBP gene for zinc binding protein	0.065	464963	TRYPSIN PRECURSOR	0.36
699	U67065	Mus musculus butyrophilin (BTN) gene, promoter region and complete cds	0.065	2132252	hypothetical protein YPL263c - yeast	3e-10
700	M64862	Rat matrix F/G mRNA, complete cds.	0.065	3420183	(AF041105) organic anion transporter protein 3 [Rattus norvegicus]	4e-19
701	K02205	Yeast (<i>S.cerevisiae</i>) transcriptional activator of amino acid-biosynthetic genes (GCN4) gene, complete cds.	0.064	<NONE>	<NONE>	<NONE>
702	X58282	Maize mRNA for a high mobility group protein	0.064	<NONE>	<NONE>	<NONE>
703	AC001545	Homo sapiens (subclone 1_f3 from P1 H69) DNA sequence	0.064	<NONE>	<NONE>	<NONE>
704	AF023461	Homo sapiens FRA3B region sequence	0.064	<NONE>	<NONE>	<NONE>
705	U50307	Caenorhabditis elegans cosmid F43H9.	0.064	<NONE>	<NONE>	<NONE>
706	U46542	Streptococcus crista HmpA gene, partial cds, putative adhesin/ABC transport system protein (scbA) gene, complete cds	0.064	1209391	(D83659) TPR protein pombe] >gi 2894282 gnl PID c1251103 (A1.021838) pre-mrna splicing factor. [Schizosaccharomyces pombe]	9.2
707	X57564	A.rusticana mRNA for neutral peroxidase	0.064	1492037	(U60315) MC094R [Molluscum contagiosum virus subtype 1]	6.9

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
708	U06986	Human alpha-2-macroglobulin receptor/lipoprotein receptor protein (A2MR/LRP) gene, exons 39-41.	0.064	100800	rab15B protein - wheat >gi 21853 (X62476) rab protein [Triticum aestivum]	5.3
709	D85773	Human CpG island sequence, clone Q28B8	0.064	2245382	(U88325) suppressor of cytokine signalling-1 [Mus musculus]	5.3
710	L06178	Apis mellifera ligustica complete mitochondrial genome	0.064	3695379	(AF096370) contains similarity to a C. elegans hypothetical protein F44G4.1 (GB:Z49910) and several yeast hypothetical proteins such as 35.1 KD protein in NAM8-GAR1 intergenic region (SP:P38805) [Arabidopsis thaliana]	3.2
711	Y16242	Triticum aestivum mRNA for beta-amylase	0.064	1175958	HYPOTHETICAL 70.5 KD PROTEIN IN AGP3-DAK3 INTERGENIC REGION >gi 1084712 pir S56201 probable membrane protein YFL054c - yeast (Saccharomyces cerevisiae) >gi 836701 gnl PID d1009825 (D50617) YFL054C	3.1
712	L81779	Homo sapiens (subclone 2_a2 from P1 H25) DNA sequence	0.064	3845169	(AE001391) phosphatase (acid phosphatase family)	0.81
713	X13826	C.reinhardtii psb1 mRNA for OEE1 protein of photosystem II (oxygen-evolving enhancer protein)	0.064	171040	(M94535) ATPase [Saccharomyces cerevisiae] cerevisiae, Peptide, 377 aa [Saccharomyces cerevisiae]	0.054
714	X06487	H.sapiens mRNA for bcl2-Ig fusion gene	0.064	2429362	(AF020261) proline rich protein [Santalum album]	0.016
715	U79638	Mus musculus cyclin-dependent kinase inhibitor protein (p15 ^{INK4b}) gene, exon 2 and partial cds	0.064	3929221	(AF082557) TRF1-interacting ankyrin-related ADP-ribose polymerase [Homo sapiens]	1e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Human T cell				
716	U39099	receptor alpha chain mRNA, partial cds	0.063	<NONE>	<NONE>	<NONE>
717	U39673	Clostridium acetobutylicum KdpC (kdpC) gene, partial cds, sensor histidine kinase homolog (kdpD) and response regulator homolog (kdpE) genes, complete cds	0.063	<NONE>	<NONE>	<NONE>
718	AL022317	Human DNA sequence from clone 140L1 on chromosome 22q13.1-13.31, complete sequence [Homo sapiens]	0.063	1931640	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]	5.2
719	U28972	Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.	0.063	4091939	(AF070704) envelope glycoprotein [Human immunodeficiency virus type 1]	5.2
720	U15159	Mus musculus limk kinase (limk) mRNA, complete cds	0.063	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	5.1
721	AF058416	Homo sapiens lipoprotein receptor-related protein (LRP1), exons 39, 40, and 41	0.063	1788123	(AE000276) orf, hypothetical protein [Escherichia coli]	4.0
722	AE001430	Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence	0.063	2244849	(Z97337) hypothetical protein	4.0

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		<i>Streptococcus</i>			(Z70203) cDNA EST	
723	L29323	pneumoniae methyl transferase gene cluster, complete sequence	0.063	3874022	EMBL:D72339 comes from this gene; cDNA EST EMBL:D75197 comes from this gene [Caenorhabditis elegans]	2.3
724	X72631	H.sapiens mRNA encoding Rev-ErbAalpha > :: emb[X72632]HSREV ERB2 H.sapiens mRNA encoding Rev-ErbAalpha (internal fragment)	0.063	3979878	(Z73105) predicted using Genefinder; cDNA EST EMBL:T01277 comes from this gene; cDNA EST EMBL:T01796 comes from this gene; cDNA EST EMBL:D32545 comes from this gene; cDNA EST EMBL:D33060 comes from this gene; cDNA EST EMBL:D...	1.7
725	U17969	Human initiation factor eIF-5A gene, complete cds.	0.063	2429509	(AF025467) contains similarity to drosophila DNA-binding protein K10 (NID:g8148) [Caenorhabditis elegans]	1.4
726	AE001000	Archaeoglobus fulgidus section 107 of 172 of the complete genome	0.063	3462802	(AF082486) nef protein [Human immunodeficiency virus type 1]	0.35
727	S80986	svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	0.063	1326288	(U58734) weak similarity to ankyrin G [Caenorhabditis elegans]	0.093
728	AF109134	Homo sapiens 7-60 mRNA, complete cds	0.063	1083764	proline-rich proteoglycan 2 precursor, parotid - rat >gi 310200 (L17318) proline-rich proteoglycan [Rattus norvegicus]	0.001
729	D87466	Human mRNA for KIAA0276 gene, partial cds	0.063	2879865	(AL021816) SPBC24E9.03c, unknown, len:251aa [Schizosaccharomyces pombe]	6e-05
730	AB018269	Homo sapiens mRNA for KIAA0726 protein, complete cds	0.063	2995865	(AF053455) tetraspan TM4SF [Homo sapiens]	2e-16
731	D86954	Cricetulus griseus mRNA for Cytochrome P-450 2A14, complete cds	0.063	2496896	HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III >gi 3874383 gnl PID e1344077 type (RING finger) [Caenorhabditis elegans]	1e-22

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-58, complete sequence	0.062	<NONE>	<NONE>	<NONE>
732	AL010232					
		Mycoplasma gallisepticum haemagglutinin precursor genes, complete cds	0.062	<NONE>	<NONE>	<NONE>
733	U90714					
		Homo sapiens clone pCL4 DNA-binding protein SOX21 (SOX21) gene, complete cds	0.062	<NONE>	<NONE>	<NONE>
734	AF107044					
		Caenorhabditis elegans Ro ribonucleoprotein autoantigen mRNA, complete cds	0.062	2983060	(AE000687) putative protein [Aquifex aeolicus]	8.6
735	L41729					
		Caenorhabditis elegans cosmid Y7A9D, complete sequence [Caenorhabditis elegans]	0.062	1176542	POTATIVE SERINE/THREONINE-PROTEIN KINASE D1044.3 IN CHROMOSOME III >gi 495684 (U00065) contains EGF-like repeats; highly similar to ZC84.1; 3' exons similar to protein kinase [Caenorhabditis elegans]	5.8
736	Z99287					
		Homo sapiens mRNA for KIAA0614 protein, partial cds	0.062	4033395	DNA GYRASE SUBUNIT B subunit [Myxococcus xanthus]	3.9
737	AB014514					
		Human germline immunoglobulin light chain variable region (lambda-IIIb subgroup) from IgM rheumatoid factor.	0.062	1914685	(Y12014) RAD23 protein, isoform II	1.3
738	L29165					
		Schistosoma japonicum Chinese clone pY6 paramyosin mRNA, partial cds.	0.062	1350800	MITOCHONDRIAL RIBOSOMAL PROTEIN S5	1.3
739	U09364					
		Triticum aestivum mRNA for beta-amylase	0.062	79834	hypothetical protein I246 (uvrA region) - Micrococcus luteus (fragment)	0.59
740	Y16242					

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Leishmania pifanoi			TROPOMYOSIN I (TMI)	
741	M97695	cysteine proteinase (cys2) gene, complete cds.	0.062	1174754	(POLYPEPTIDE 49) >gi 320989 pir A60607 tropomyosin - fluke	0.018
742	U67526	Methanococcus jannaschii section 68 of 150 of the complete genome	0.062	1330345	(U58755) coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	1e-40
743	Z78414	Caenorhabditis elegans cosmid W09D12, complete sequence [Caenorhabditis elegans]	0.061	<NONE>	<NONE>	<NONE>
744	Y13606	Mus musculus gene encoding filensin, exons 6, 7	0.061	2314715	(AE000651) H. pylori predicted coding region HP1527	4.9
745	J04374	Eggplant mosaic virus genome.	0.061	141449	HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556 >gi 80759 pir JQ0431 hypothetical 35.5K protein - Streptomyces fradiae transposon Tn4556	3.8
746	AB022200	Marine obligately oligotrophic bacterium POO-10 DNA for 16S ribosomal RNA, partial sequence	0.061	3983593	(AB000307) transcarboxylase-beta	2.2
747	X54250	Rat mRNA for zinc finger protein AT-BP2, partial cds	0.061	1377886	(L46815) DNA binding protein Rc [Mus musculus]	0.98
748	X69942	M.musculus mRNA of enhancer-trap-locus 1	0.061	2983969	(AE000748) putative protein [Aquifex aeolicus]	0.57
749	AJ223206	Mus musculus mRNA for scrapie responsive protein 1	0.061	4204265	(AC005223) 45643 [Arabidopsis thaliana]	5e-31
750	Y10205	H.sapiens mRNA for CD88 protein	0.060	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
751	U79260	Human clone 23745 mRNA, complete cds	0.060	<NONE>	<NONE>	<NONE>
752	X07453	Plasmodium falciparum 11-1 gene part 1	0.060	<NONE>	<NONE>	<NONE>
753	U57502	Rattus norvegicus protein tyrosine phosphatase delta gene, catalytic domain, partial cds.	0.060	3452285	(AF044915) polar tube protein PTP55 precursor	0.28
754	X68359	M.fascicularis gene for apolipoprotein C-III	0.060	730843	SHUTTLE CRAFT PROTEIN >gi 487400	2e-04
755	X51634	Pseudomonas braB gene for branched chain amino acid transport carrier (LIV-II)	0.059	1835622	(U85718) CCML [Pseudomonas putida GB-1]	8.1
756	AF072405	Gossypium hirsutum cotton fiber expressed protein 2 (CFE2) mRNA, complete cds	0.059	423766	alkaline phosphatase, 145K - Synechococcus sp.	4.7
757	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.056	2662481	(AF034859) juvenile hormone resistance protein	3.3
758	AF093268	Rattus norvegicus homer-1c mRNA, complete cds	0.054	547847	LECTIN PRECURSOR	7.0
759	X61046	Hydra N-COL 2 mRNA for mini-collagen, partial cds	0.053	<NONE>	<NONE>	<NONE>
760	AJ005813	Arabidopsis thaliana mRNA for neoxanthin cleavage enzyme	0.052	<NONE>	<NONE>	<NONE>
761	S79843	{random amplified hybridization microsatellite RAHM} [Beta vulgaris=sugar beets, Genomic, 537 nt]	0.025	1730145	GAMETOGENESIS EXPRESSED PROTEIN GEG-154 >gi 2137331 pir I48361 gene GEG-154 protein - mouse >gi 550123 (X71642) pid:g550123 [Mus musculus]	2e-16

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mouse mRNA for				
762	AB000096	GATA-2 protein, complete cds	0.023	<NONE>	<NONE>	<NONE>
763	Z62366	H.sapiens CpG DNA, clone 67h7, forward read cpg67h7.ft1a	0.023	3123312	ZINC FINGER PROTEIN 142 (KIAA0236) to Human zinc finger protein(ZNF142) [Homo sapiens]	5.9
764	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2 through 8.	0.023	80636	hypothetical 67K protein - Mycobacterium fortuitum plasmid pAL5000 >gi 149986 (M60875) ORF2	3.4
765	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.023	3114665	(AF061267) inner membrane component HtxE [Pseudomonas stutzeri]	3.4
766	X98890	S.tuberosum mRNA for inorganic phosphate transporter, StPT1	0.023	683532	(X02155) thyroglobulin [Bos taurus]	1.1
767	U58835	Dissostichus mawsoni preprotrypsin gene, complete cds	0.022	<NONE>	<NONE>	<NONE>
768	AJ009630	Glomus versiforme chitin synthase gene (clone Gvchs3)	0.022	<NONE>	<NONE>	<NONE>
769	J04040	Human glucagon mRNA, complete cds.	0.022	<NONE>	<NONE>	<NONE>
770	X74908	L.esculentum Asr3 gene	0.022	<NONE>	<NONE>	<NONE>
771	L07293	Shigella dysenteriae O-antigen polysaccharide biosynthesis rfbX, O-antigen polymerase (rfc), rhamnosyl transferase I and II (rfbR and rfbQ) and rfbD genes, complete cds.	0.022	<NONE>	<NONE>	<NONE>

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Mus musculus				
772	AF040094	inositol polyphosphate 5-phosphatase II (INPP5P) mRNA, complete cds	0.022	<NONE>	<NONE>	<NONE>
773	X76776	H.sapiens HLA-DMB gene	0.022	<NONE>	<NONE>	<NONE>
774	AE001521	Helicobacter pylori, strain J99 section 82 of 132 of the complete genome	0.022	<NONE>	<NONE>	<NONE>
775	X16004	A.longa rbcL, rpl5, rps8, rpl36, rps14, rps2, trnI, trnF, trnC and rpoB (partial) genes > :: emb[X75651]ALRIBP A.longa plastid genes for ribosomal proteins, tRNAs, RNA polymerase subunit beta and rubisco large subunit	0.022	<NONE>	<NONE>	<NONE>
776	Y12707	Lactococcus lactis cremoris plasmid pHW393 DNA, rlladii, mlladii genes	0.022	<NONE>	<NONE>	<NONE>
777	U27118	Arabidopsis thaliana glutamyl-tRNA reductase	0.022	<NONE>	<NONE>	<NONE>
778	Z96622	H.sapiens telomeric DNA sequence, clone SPTEL002, read SPTELOO002.seq	0.022	191333	(J05503) carbamoyl-phosphate synthetase (E.C.6.3.5.5)	9.8
779	D83984	Sulculus diversicolor DNA for IDO-like myoglobin, complete cds	0.022	1078509	probable membrane protein YDR018c - yeast	9.7
780	Z77952	H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA-4A3	0.022	4204206	(AB022786) N-acetyl-beta-D-glucosaminidase [Enterobacter sp.]	7.5

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		Xenopus laevis				
781	M10217	mitochondrial DNA, complete genome.	0.022	2145763	B2168_C2_205 protein - Mycobacterium leprae	7.3
782	M55147	Pea chloroplast glyceraldehyde-3-phosphate dehydrogenase (Gpb1) gene, complete cds.	0.022	417308	PROBABLE HELICASE MOT1 Mot1p is a probable helicase essential for vegetative growth on rich glucose medium at 30 degree C: Swiss-Prot Accession number P32333; similar to S. cerevisiae RAD26 gene product: Swiss-Prot Accession number P40352	4.2
783	X58839	Acholeplasma virus MV-L1 DNA for complete circular genome	0.022	3273189	(AB008757) subunit II of c(o/b)3-type cytochrome c oxidase [Bacillus stearothermophilus]	4.1
784	M26185	Mouse c-myb oncogene, exon 1 and exon 2 (partial).	0.022	138592	VITELLOGENIN I PRECURSOR (YOLK PROTEIN I) >gi 72270 pir VJFF1 vitellogenin I precursor unnamed protein product [Drosophila melanogaster]	2.5
785	AF061195	Streptomyces albus valine dehydrogenase (Vdh) gene, complete cds	0.022	2088768	(AF003145) B0414.8 gene product [Caenorhabditis elegans]	0.86
786	AF053622	Homo sapiens alpha 1,2-mannosidase IB gene, exon 9	0.022	1352361	EARLY GROWTH RESPONSE PROTEIN 1 fish >gi 531456 (U12895) egr1 [Danio rerio] rerio]	0.36
787	Z71500	S.cerevisiae chromosome XIV reading frame ORF YNL224c	0.022	1708875	PUTATIVE TUMOR SUPPRESSOR LUCA15 sapiens]	0.16
788	D10471	Herpes simplex virus type 2 genomic DNA for 0.74-0.84 region, complete cds	0.022	3132276	(AB011486) short ORF [TT virus]	0.13
789	U43082	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds	0.022	3319720	(AL031035) putative aldehyde dehydrogenase [Streptomyces coelicolor]	0.011

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		H.sapiens simple tandem repeat DNA (clone wg3a6)				
790	X86913		0.021	<NONE>	<NONE>	<NONE>
		Mus musculus Pontin52 mRNA, complete cds				
791	AF100694		0.021	<NONE>	<NONE>	<NONE>
		Nannostomus sp. large subunit rRNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.				
792	U34016		0.021	<NONE>	<NONE>	<NONE>
		Yeast mitochondrial genes for 15S rRNA and tRNA-Tip				
793	X00845		0.021	<NONE>	<NONE>	<NONE>
		Homo sapiens gene for CC chemokine PARC precursor, complete cds				
794	AB012113		0.021	<NONE>	<NONE>	<NONE>
		Daucus carota globulin-like protein (Gca8) gene, complete cds				
795	U62395		0.021	<NONE>	<NONE>	<NONE>
		P.falciparum actin II gene, complete cds.			(AF004835) tyrocidine synthetase 3 [Brevibacillus brevis]	
796	M22718		0.021	2623773		8.8
		Arabidopsis thaliana glutamyl-tRNA reductase			(AJ006631) cysteine-rich secretory protein-1 [Equus caballus]	
797	U27118		0.021	3549885		8.8
		H.sapiens CLN3 gene, complete CDS			(S52010) orf1 5' of EpoR [mice, Peptide, 85 aa] [Mus sp.]	
798	X99832		0.021	262249		8.7
		Homo sapiens TRAIL receptor 2 mRNA, complete cds			SUCCINYL-COA:COENZYME A TRANSFERASE transferase [Clostridium kluyveri]	
799	AF016266		0.021	729048		8.7
		Human DNA sequence from PAC 179I15, BRCA2 gene region chromosome 13q12-13 contains lactase-phlorizin hydrolase (LCT)			LIPOPOLYSACCHARIDE 1,2-N-ACETYLGLUCOSAMINE TRANSFERASE >gi 466761 (U00039) rfaK [Escherichia coli] >gi 1790053 (AE000440) probably hexose transferase; lipopolysaccharide core biosynthesis	
800	Z92541		0.021	585820		5.3

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
		dopamine D2				
801	S58588	receptor [human, brain, Genomic, 3794 nt. segment 4 of 5]	0.021	2677620	(Y08029) NAD(P)(+)-arginine ADP-ribosyltransferase [Oryctolagus cuniculus]	5.1
802	M60522	Rat nerve growth factor-inducible protein (VGF) gene, complete cds.	0.021	4103934	(AF030050) replication factor C [Rattus norvegicus]	3.1
803	AF045654	Gallus gallus neuregulin beta-1a mRNA, complete cds	0.021	2746829	(AF040647) No definition line found [Caenorhabditis elegans]	3.0
804	M69023	Human globin gene.	0.021	3880259	(Z82056) T26H5.8 [Caenorhabditis elegans] >gi 3880787 gnl PID e1350288 (AL032620) T26H5.8	2.4
805	Z65960	H.sapiens CpG DNA, clone 69d2, reverse read cpg69d2.rt1b.	0.021	1707245	(U80845) similar to family 1 of G-protein coupled receptors [Caenorhabditis elegans]	0.79
806	X97073	A.oligospora gene encoding lectin	0.021	116949	CORE ANTIGEN >gi 73601 pir NKVLC2 core antigen - woodchuck hepatitis virus 2 >gi 336135	0.47
807	X56491	D. melanogaster mRNA for gene containing opa repetitive element	0.021	2842750	HOMEBOX PROTEIN DLX-7 >gi 1620520	0.16
808	L78760	Homo sapiens (subclone 1_f6 from P1 H31) DNA sequence	0.021	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.15
809	AB007864	Homo sapiens KIAA0404 mRNA, partial cds	0.021	118144	CYSTEINE SYNTHASE A (O-ACETYL SERINE SULFHYDRYLASE A) (O-ACETYL SERINE (THIOL)-LYASE A) (CSASE A) >gi 68323 pir SYEBAC cysteine synthase (EC 4.2.99.8) A - Salmonella typhimurium >gi 153935 (M21450) cysK protein [Salmonella typhimurium]	0.12
810	AL021932	Mycobacterium tuberculosis H37Rv complete genome; segment 22/162	0.021	2909514	(AL021932) hypothetical protein Rv0439c	7e-10

SEQ ID	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
811	U89991	Hypocrea jecorina mannose-1-phosphate guanylyltransferase (MPG1) mRNA, complete cds	0.021	3581924	(AL031538) mannose-1-phosphate guanylyltransferase [Schizosaccharomyces pombe]	6e-20
812	X00641	Sugar beet mitochondrial minicircle pO sequence	0.020	<NONE>	<NONE>	<NONE>
813	Z50097	D.melanogaster mRNA for hdc protein.	0.020	<NONE>	<NONE>	<NONE>
814	AF044866	Phoebis sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs	0.020	<NONE>	<NONE>	<NONE>
815	AF074386	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
816	AF027174	Arabidopsis thaliana cellulose synthase catalytic subunit (Ath-B) mRNA, complete cds	0.020	<NONE>	<NONE>	<NONE>
817	AE001405	Plasmodium falciparum chromosome 2, section 42 of 73 of the complete sequence	0.020	2196776	(AF003342) bunched gene product [Drosophila melanogaster]	8.4
818	AF074387	Sambucus nigra hevein-like protein mRNA, complete cds	0.020	627071	histidine-rich protein - Plasmodium lophurae	2.8